



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 04:26 pm BST

PDB ID : 6TH6 / pdb_00006th6
EMDB ID : EMD-10503
Title : Cryo-EM Structure of T. kodakarensis 70S ribosome
Authors : Matzov, D.; Sas-Chen, A.; Thomas, J.M.; Santangelo, T.; Meier, J.L.;
Schwartz, S.; Shalev-Benami, M.
Deposited on : 2019-11-18
Resolution : 2.55 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

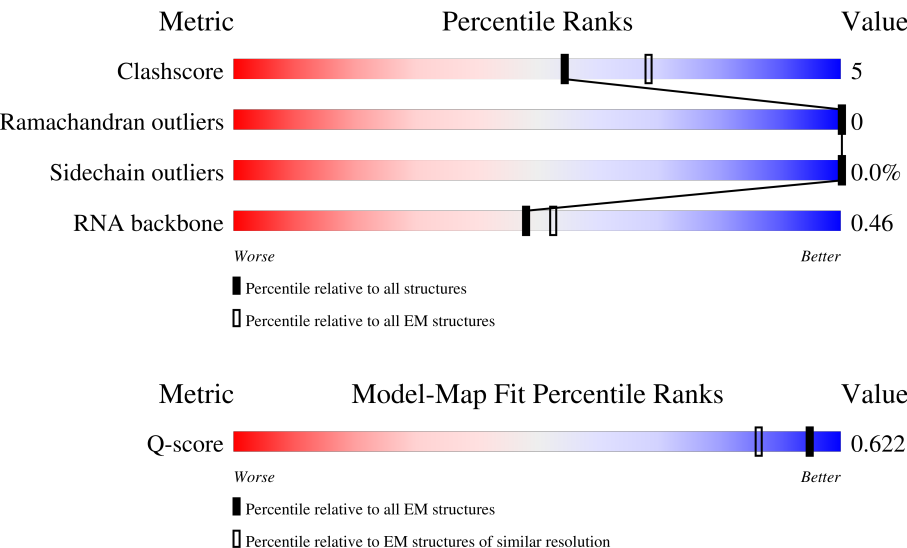
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7475 (2.05 - 3.05)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Aa	1498	11% 69% 24% . .
2	Ab	201	25% 85% 12% .
3	Ac	209	81% 85% 6% 9%

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Mol	Chain	Length	Quality of chain
4	Ad	200	
5	Ae	180	
6	Af	243	
7	Ag	235	
8	Ah	125	
9	Ai	215	
10	Aj	130	
11	Ak	130	
12	Al	135	
13	Am	102	
14	An	140	
15	Ao	147	
16	Ap	149	
17	Aq	151	
18	Ar	56	
19	As	114	
20	At	67	
21	Au	133	
22	Av	150	
23	Aw	98	
24	Ax	65	
25	Ay	70	
26	Az	62	
27	BA	3037	
28	BB	126	

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Mol	Chain	Length	Quality of chain
29	BC	239	
30	BD	346	
31	BE	255	
32	BF	183	
33	BG	184	
34	BH	123	
34	BI	123	
35	BJ	182	
36	BK	142	
37	BL	141	
38	BM	83	
38	BN	83	
39	BO	148	
40	BP	194	
41	BQ	201	
42	BR	121	
43	BS	150	
44	BT	77	
45	BU	98	
46	BV	156	
47	BW	86	
48	BX	121	
49	BY	67	
50	BZ	66	
51	Ba	155	

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Mol	Chain	Length	Quality of chain
52	Bb	102	
53	Bc	90	
54	Bd	125	
55	Be	90	
56	Bg	86	
57	Bh	63	
58	Bi	51	
59	Bj	51	
60	Bk	37	
61	Bl	94	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 161508 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	1463	Total	C	N	O	P	0	0
			31499	14027	5837	10172	1463		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	196	Total	C	N	O	S	0	0
			1580	1021	272	284	3		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ac	191	Total	C	N	O	S	0	0
			1513	967	276	267	3		

- Molecule 4 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ad	190	Total	C	N	O	S	0	0
			1550	997	277	273	3		

- Molecule 5 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ae	174	Total	C	N	O	S	0	0
			1454	912	287	253	2		

- Molecule 6 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Af	241	Total	C	N	O	S	0	0
			1945	1256	348	336	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ag	223	Total	C	N	O	S	0	0
			1753	1107	327	312	7		

- Molecule 8 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Ah	123	Total	C	N	O	S	0	0
			952	599	179	172	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ai	213	Total	C	N	O	S	0	0
			1706	1082	316	300	8		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Aj	129	Total	C	N	O	S	0	0
			1020	662	176	180	2		

- Molecule 11 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ak	125	Total	C	N	O		0	0
			982	615	198	169			

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Al	133	Total	C	N	O	S	0	0
			1054	656	205	188	5		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Am	100	Total	C	N	O	S	0	0
			803	498	154	148	3		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	An	127	Total	C	N	O	S	0	0
			953	587	190	173	3		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ao	143	Total	C	N	O	S	0	0
			1122	712	216	192	2		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ap	135	Total	C	N	O	S	0	0
			1090	691	214	181	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aq	149	Total	C	N	O	S	0	0
			1217	776	233	206	2		

- Molecule 18 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ar	54	Total	C	N	O	S	0	0
			447	284	92	65	6		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	As	107	Total	C	N	O	S	0	0
			868	554	160	151	3		

- Molecule 20 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	At	64	Total	C	N	O	S	0	0
			538	338	103	95	2		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Au	116	Total	C	N	O	S	0	0
			952	608	175	163	6		

- Molecule 22 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Av	149	Total	C	N	O	S	0	0
			1216	788	215	213			

- Molecule 23 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Aw	95	Total	C	N	O	S	0	0
			777	497	131	146	3		

- Molecule 24 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ax	61	Total	C	N	O	S	0	0
			461	294	83	79	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ax	64	GLU	LEU	conflict	UNP Q5JE50
Ax	65	LEU	GLU	conflict	UNP Q5JE50

- Molecule 25 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Ay	64	Total	C	N	O	S	0	0
			499	307	99	93			

- Molecule 26 is a protein called Predicted zinc-ribbon RNA-binding protein involved in translation.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Az	55	Total	C	N	O	S	0	0
			426	269	74	75	8		

- Molecule 27 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	BA	2934	Total	C	N	O	P	S	0	0
			63188	28147	11754	20352	2934	1		

- Molecule 28 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BB	125	Total	C	N	O	P	0	0
			2678	1191	492	870	125		

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BC	237	Total	C	N	O	S	0	0
			1820	1150	356	311	3		

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BD	344	Total	C	N	O	S	0	0
			2746	1765	505	469	7		

- Molecule 31 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BE	255	Total	C	N	O	S	0	0
			2026	1286	389	347	4		

- Molecule 32 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BF	166	Total	C	N	O	S	0	0
			1338	839	258	234	7		

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BG	183	Total	C	N	O	S	0	0
			1463	942	253	266	2		

- Molecule 34 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BH	121	Total	C	N	O	S	0	0
			928	591	154	180	3		
34	BI	121	Total	C	N	O	S	0	0
			928	591	154	180	3		

- Molecule 35 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BJ	168	Total	C	N	O	S	0	0
			1378	877	258	236	7		

- Molecule 36 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BK	142	Total	C	N	O	S	0	0
			1146	731	213	198	4		

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	140	Total	C	N	O	S	0	0
			1055	658	214	180	3		

- Molecule 38 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BM	81	Total	C	N	O	S	0	0
			610	382	119	108	1		
38	BN	81	Total	C	N	O	S	0	0
			610	382	119	108	1		

- Molecule 39 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	148	Total	C	N	O	S	0	0
			1162	740	221	198	3		

- Molecule 40 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	193	Total	C	N	O	S	0	0
			1582	1010	316	250	6		

- Molecule 41 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	164	Total	C	N	O	S	0	0
			1314	841	243	228	2		

- Molecule 42 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	120	Total	C	N	O	S	0	0
			959	601	187	169	2		

- Molecule 43 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	146	Total	C	N	O	S	0	0
			1200	753	246	194	7		

- Molecule 44 is a protein called 50S ribosomal protein L18Ae.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BT	74	Total	C	N	O	0	0
			624	399	113	112		

- Molecule 45 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BU	96	Total	C	N	O	S	0	0
			784	502	158	123	1		

- Molecule 46 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	154	Total	C	N	O	S	0	0
			1234	777	242	211	4		

- Molecule 47 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	85	Total	C	N	O	S	0	0
			683	438	119	123	3		

- Molecule 48 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	120	Total	C	N	O	S	0	0
			991	628	188	170	5		

- Molecule 49 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	62	Total	C	N	O	S	0	0
			524	334	99	85	6		

- Molecule 50 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	60	Total	C	N	O	S	0	0
			506	314	98	90	4		

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ba	154	Total	C	N	O	S	0	0
			1242	788	235	214	5		

- Molecule 52 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bb	96	Total	C	N	O	S	0	0
			730	473	123	133	1		

- Molecule 53 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Bc	89	Total	C	N	O	0	0
			721	463	140	118		

- Molecule 54 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bd	124	Total	C	N	O	S	0	0
			1022	650	208	162	2		

- Molecule 55 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Be	89	Total	C	N	O	S	0	0
			728	454	155	110	9		

- Molecule 56 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bg	84	Total	C	N	O	S	0	0
			630	392	132	101	5		

- Molecule 57 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Bh	62	Total	C	N	O	S	0	0
			512	314	118	75	5		

- Molecule 58 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Bi	50	Total	C	N	O	S	0	0
			432	276	97	59			

- Molecule 59 is a protein called 50S ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Bj	47	Total	C	N	O	S	0	0
			373	233	79	56	5		

- Molecule 60 is a protein called LSU ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Bk	36	Total	C	N	O	S	0	0
			345	218	86	39	2		

- Molecule 61 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bl	93	Total	C	N	O	S	0	0
			778	494	160	119	5		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	Ag	1	Total 1	Zn 1	0
62	Ar	1	Total 1	Zn 1	0
62	As	1	Total 1	Zn 1	0
62	Ax	1	Total 1	Zn 1	0
62	Az	2	Total 2	Zn 2	0
62	BY	1	Total 1	Zn 1	0
62	Be	1	Total 1	Zn 1	0
62	Bg	1	Total 1	Zn 1	0
62	Bh	1	Total 1	Zn 1	0
62	Bj	1	Total 1	Zn 1	0
62	Bl	1	Total 1	Zn 1	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms		AltConf
63	Aa	153	Total 153	O 153	0
63	Ae	1	Total 1	O 1	0
63	Af	5	Total 5	O 5	0
63	Ag	1	Total 1	O 1	0
63	Ai	1	Total 1	O 1	0
63	Aj	1	Total 1	O 1	0
63	Ak	2	Total 2	O 2	0
63	Al	2	Total 2	O 2	0
63	An	1	Total 1	O 1	0

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Mol	Chain	Residues	Atoms		AltConf
63	Ao	2	Total 2	O 2	0
63	Ap	1	Total 1	O 1	0
63	Aq	5	Total 5	O 5	0
63	Av	1	Total 1	O 1	0
63	Az	1	Total 1	O 1	0
63	BA	1674	Total 1674	O 1674	0
63	BB	7	Total 7	O 7	0
63	BC	29	Total 29	O 29	0
63	BD	30	Total 30	O 30	0
63	BE	24	Total 24	O 24	0
63	BF	1	Total 1	O 1	0
63	BH	1	Total 1	O 1	0
63	BJ	4	Total 4	O 4	0
63	BK	7	Total 7	O 7	0
63	BL	8	Total 8	O 8	0
63	BN	1	Total 1	O 1	0
63	BO	19	Total 19	O 19	0
63	BP	23	Total 23	O 23	0
63	BQ	5	Total 5	O 5	0
63	BR	1	Total 1	O 1	0
63	BS	12	Total 12	O 12	0

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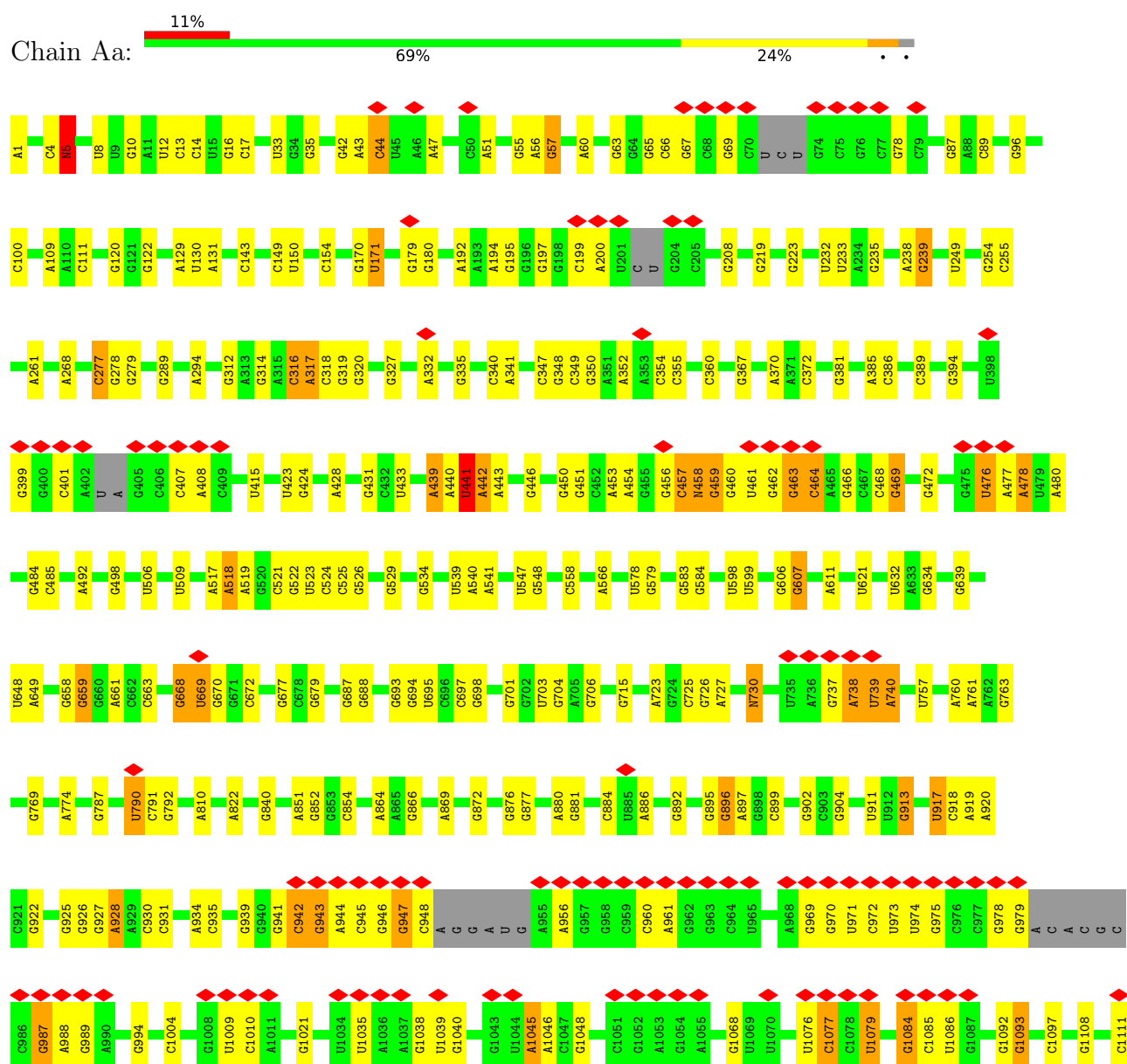
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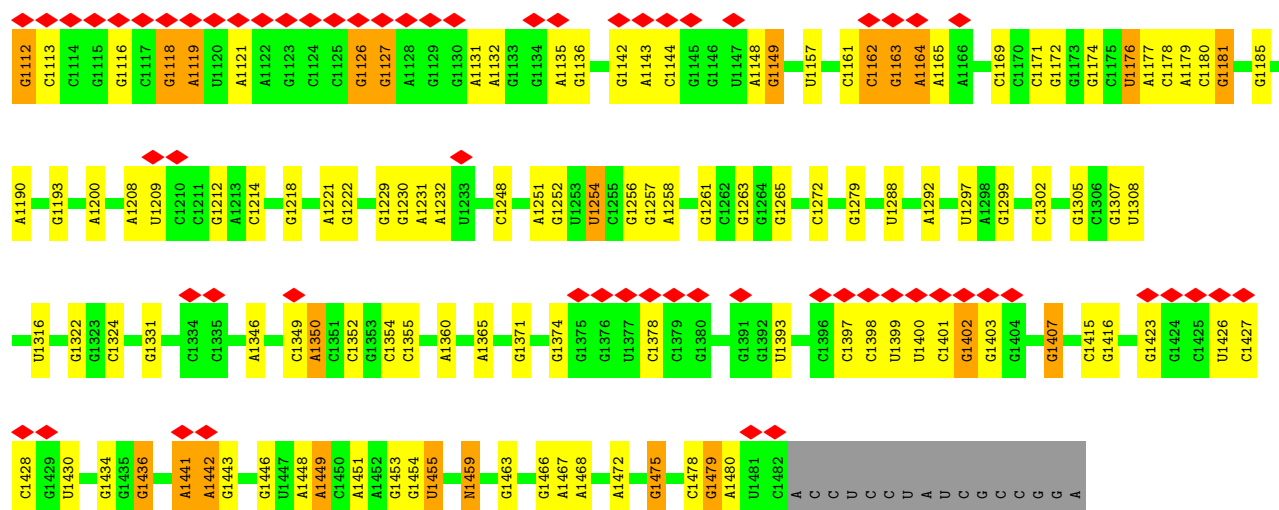
Mol	Chain	Residues	Atoms		AltConf
63	BV	17	Total 17	O 17	0
63	BW	3	Total 3	O 3	0
63	BX	7	Total 7	O 7	0
63	BY	5	Total 5	O 5	0
63	BZ	3	Total 3	O 3	0
63	Ba	6	Total 6	O 6	0
63	Bb	1	Total 1	O 1	0
63	Bc	7	Total 7	O 7	0
63	Bd	12	Total 12	O 12	0
63	Be	7	Total 7	O 7	0
63	Bg	6	Total 6	O 6	0
63	Bh	18	Total 18	O 18	0
63	Bi	5	Total 5	O 5	0
63	Bk	6	Total 6	O 6	0
63	Bl	3	Total 3	O 3	0

3 Residue-property plots

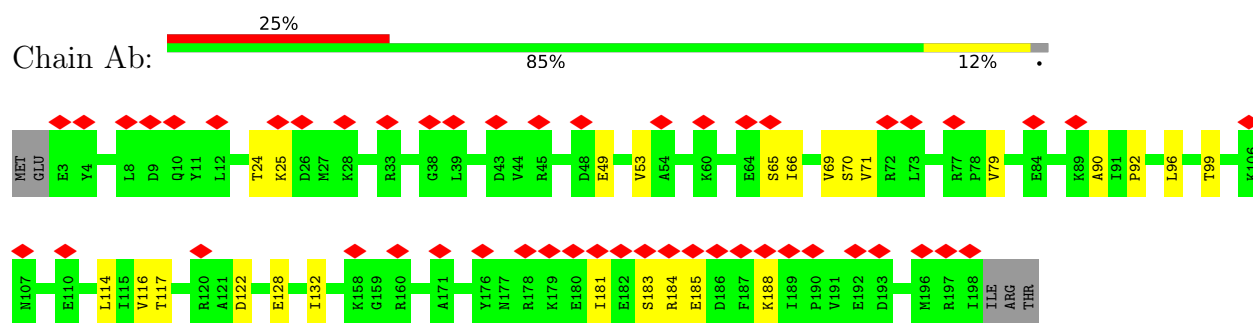
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA

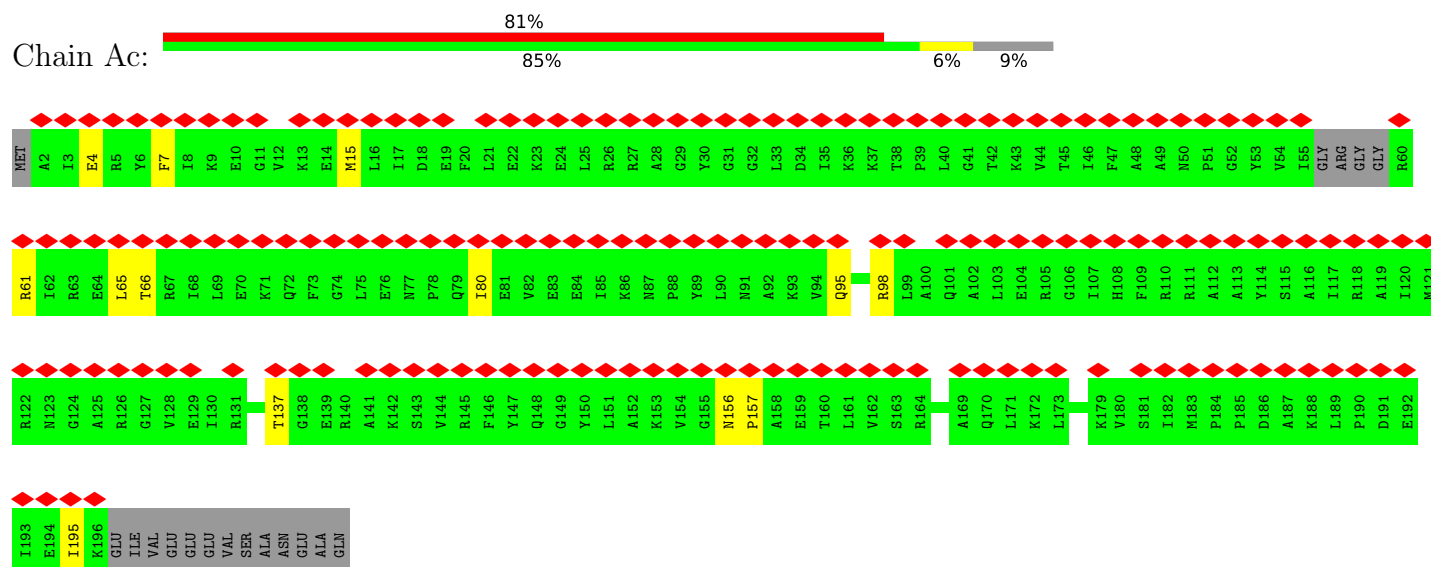




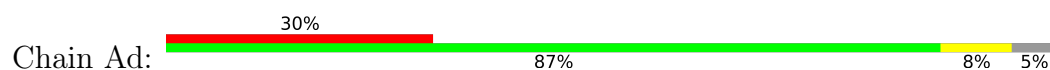
• Molecule 2: 30S ribosomal protein S2

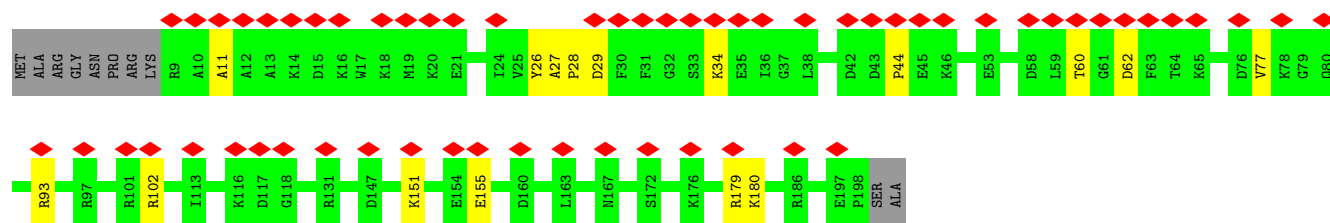


• Molecule 3: 30S ribosomal protein S3

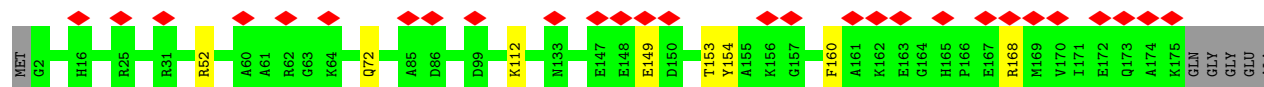


• Molecule 4: 30S ribosomal protein S3Ae

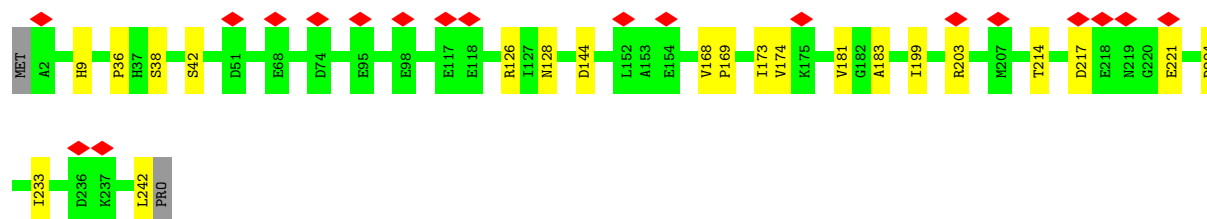
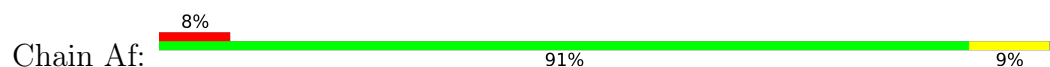




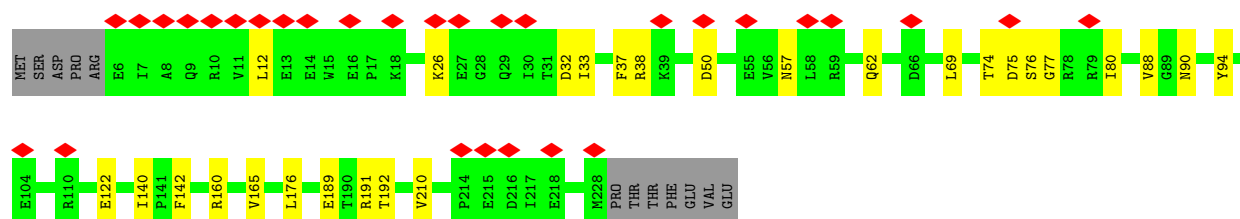
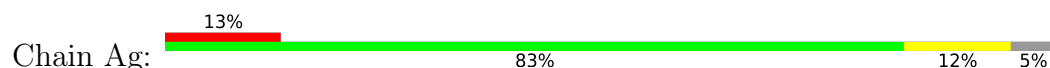
• Molecule 5: 30S ribosomal protein S4



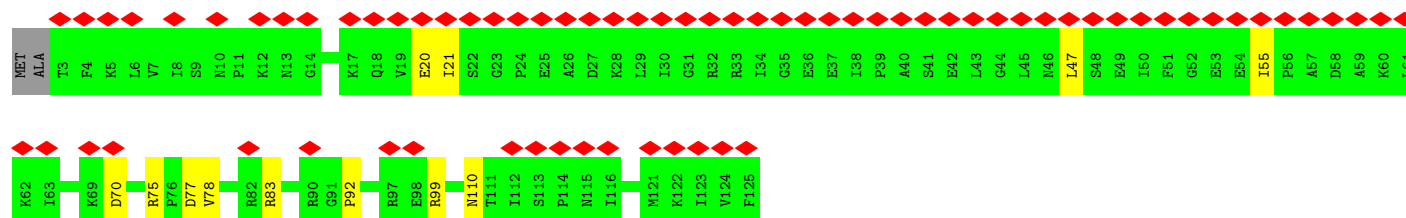
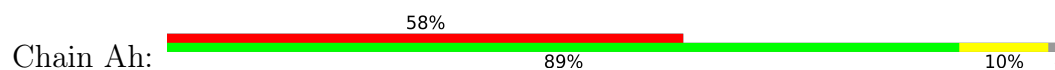
• Molecule 6: 30S ribosomal protein S4e



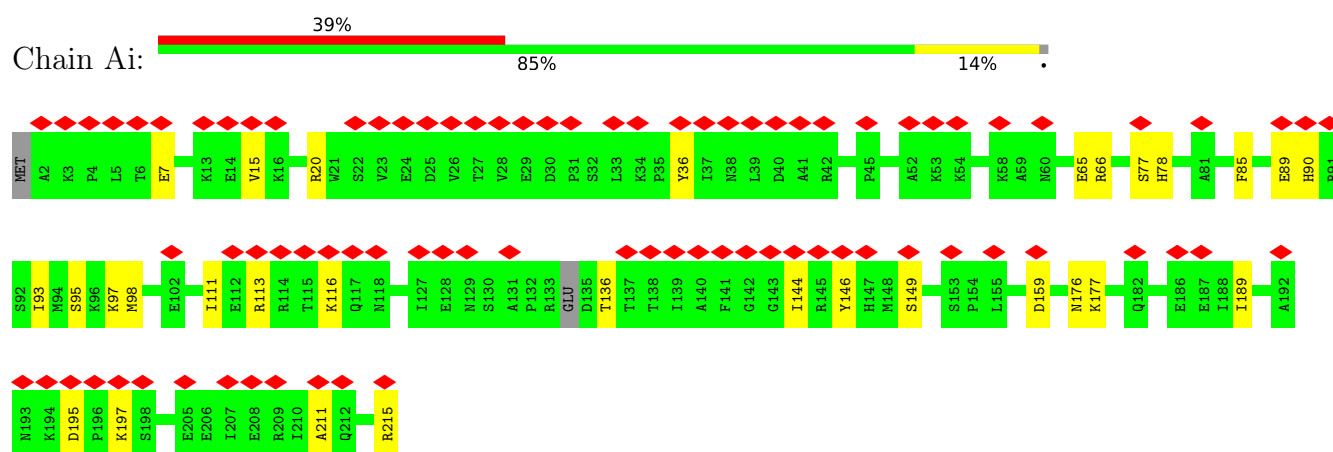
• Molecule 7: 30S ribosomal protein S5



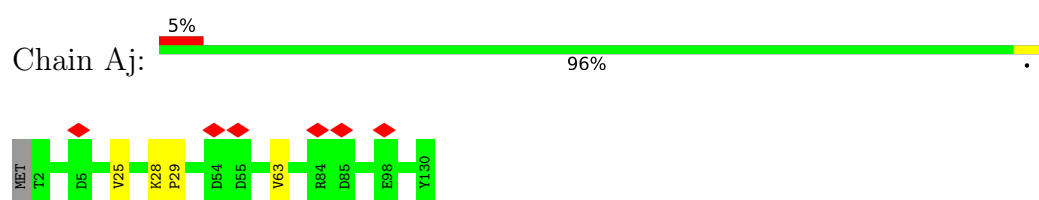
• Molecule 8: 30S ribosomal protein S6e



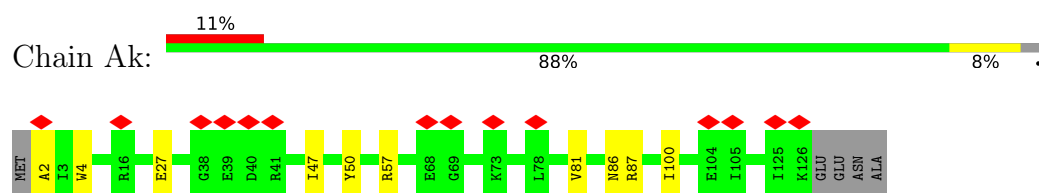
• Molecule 9: 30S ribosomal protein S7



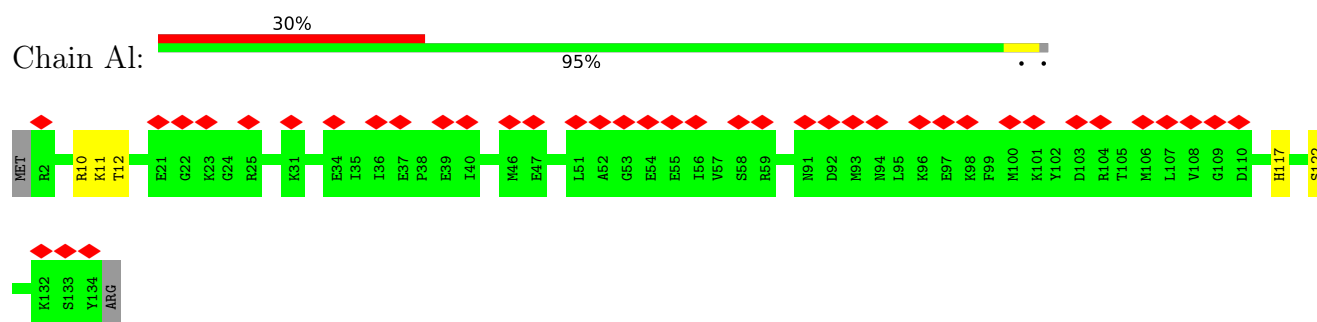
- Molecule 10: 30S ribosomal protein S8



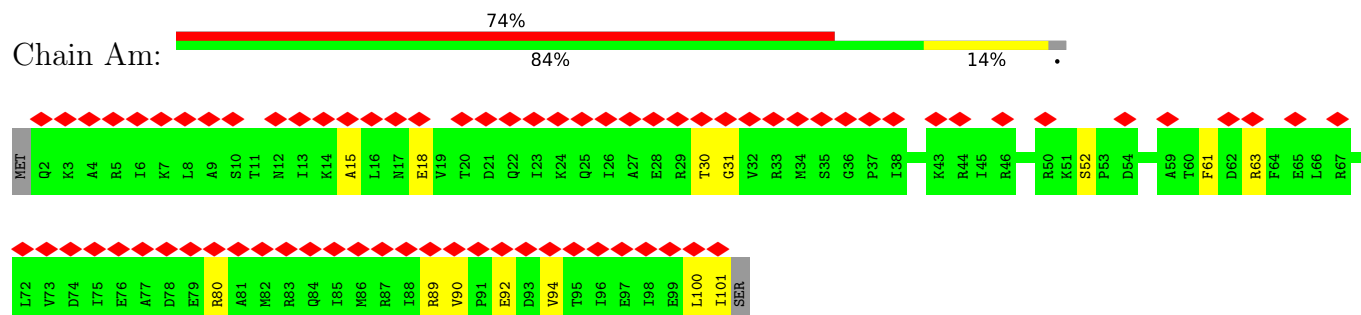
- Molecule 11: 30S ribosomal protein S8e



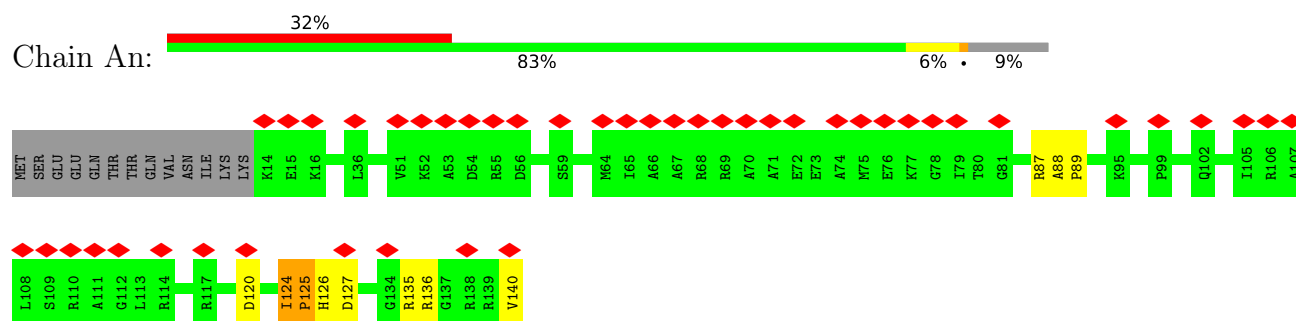
- Molecule 12: 30S ribosomal protein S9



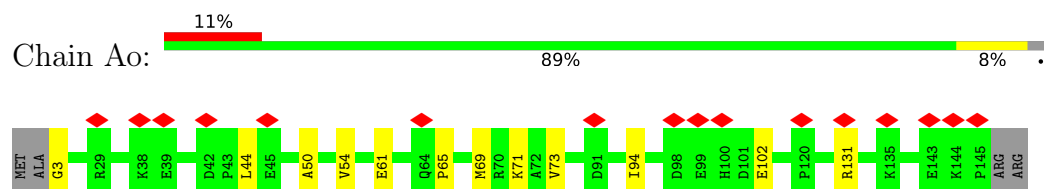
- Molecule 13: 30S ribosomal protein S10



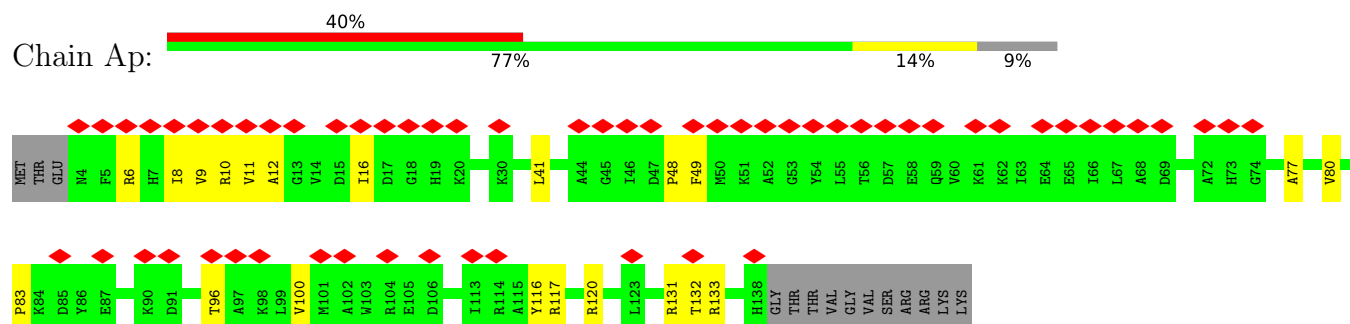
- Molecule 14: 30S ribosomal protein S11



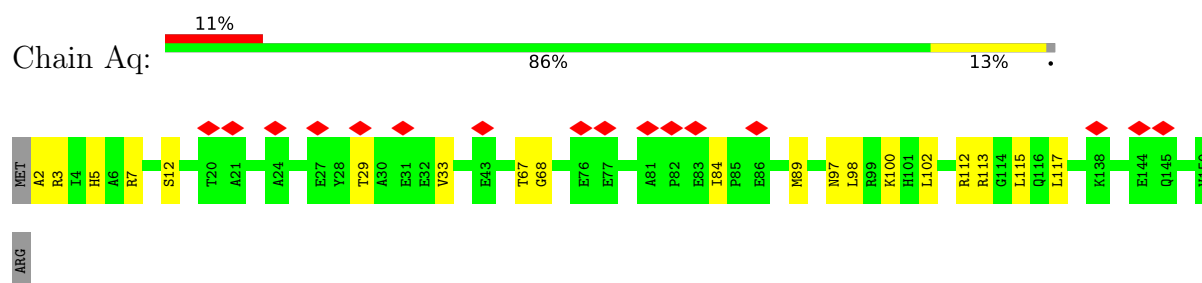
- Molecule 15: 30S ribosomal protein S12



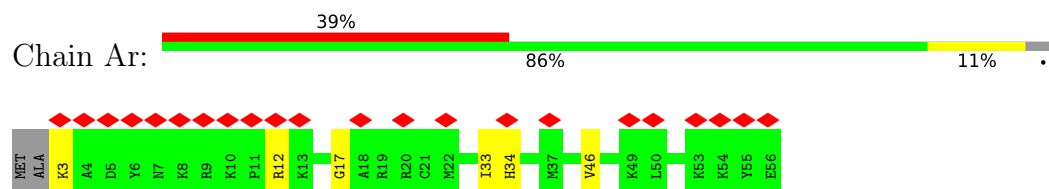
- Molecule 16: 30S ribosomal protein S13



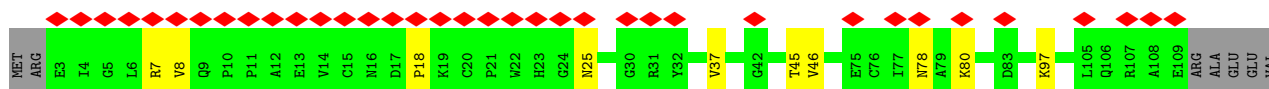
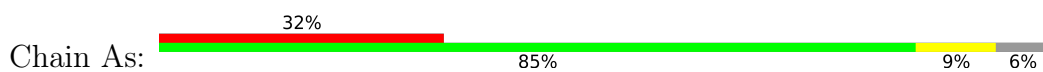
- Molecule 17: 30S ribosomal protein S15



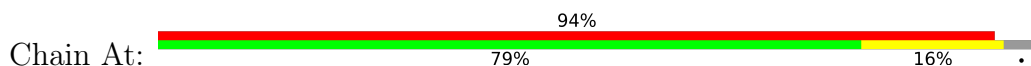
- Molecule 18: 30S ribosomal protein S14 type Z



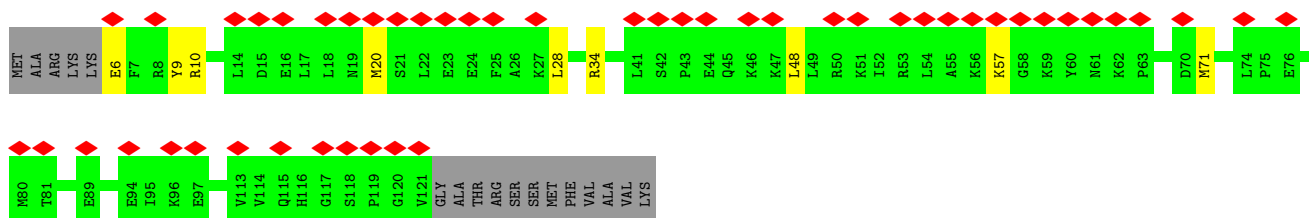
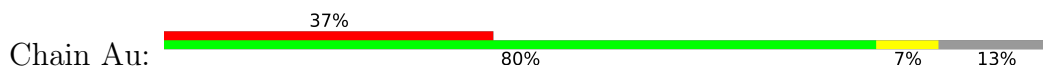
- Molecule 19: 30S ribosomal protein S17



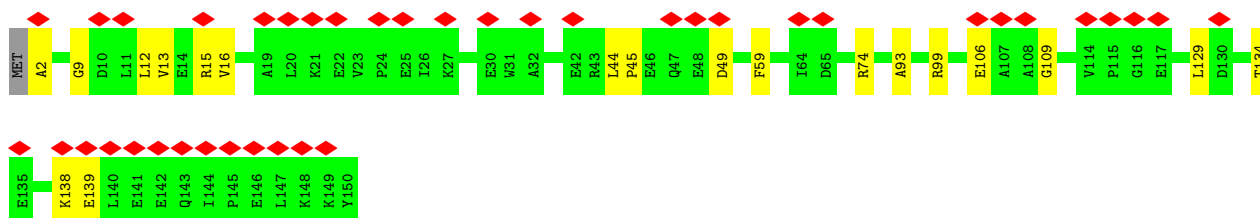
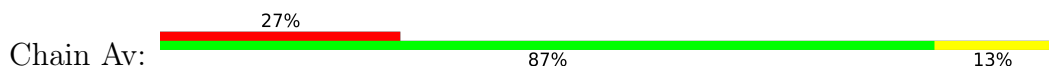
• Molecule 20: 30S ribosomal protein S17e



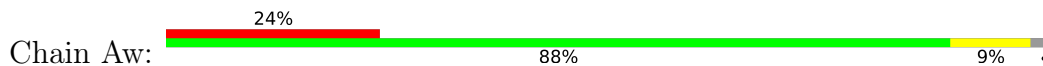
• Molecule 21: 30S ribosomal protein S19



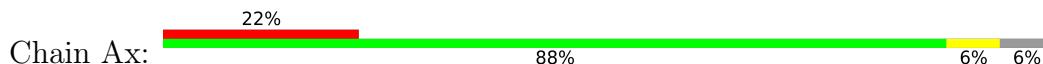
• Molecule 22: 30S ribosomal protein S19e

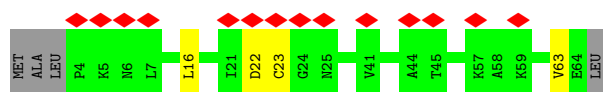


• Molecule 23: 30S ribosomal protein S24e

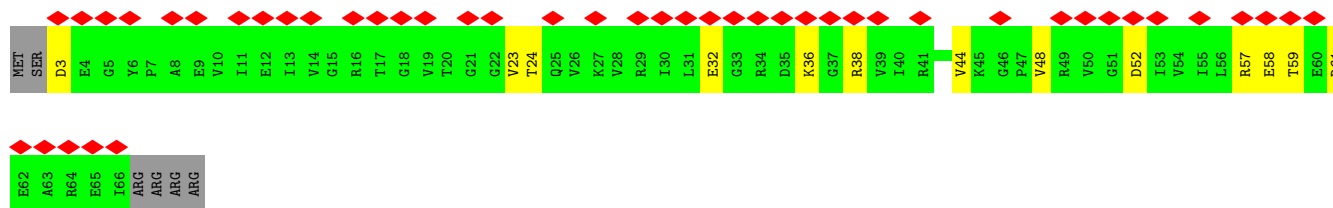
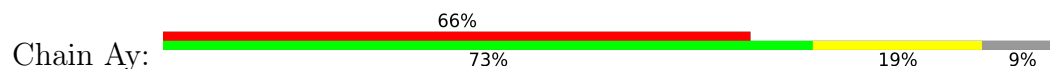


• Molecule 24: 30S ribosomal protein S27e

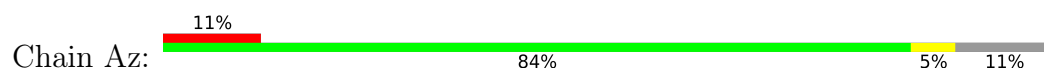




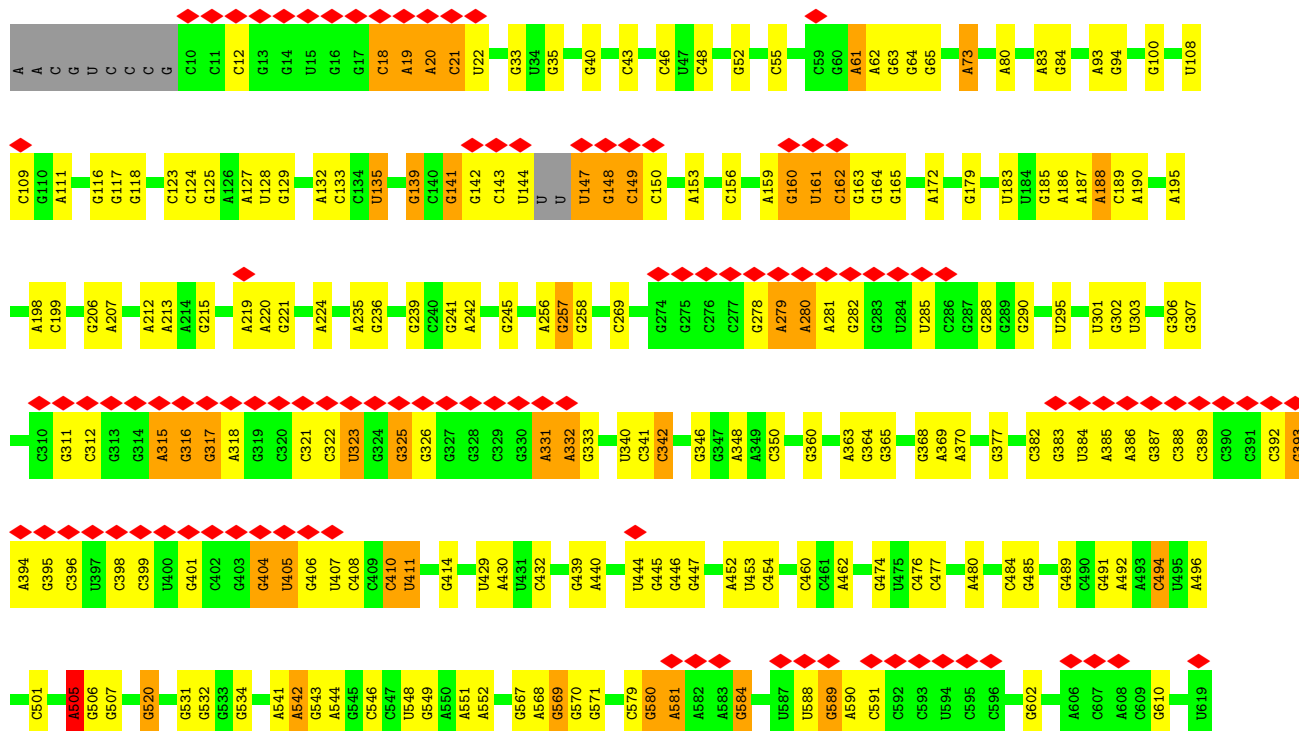
- Molecule 25: 30S ribosomal protein S28e



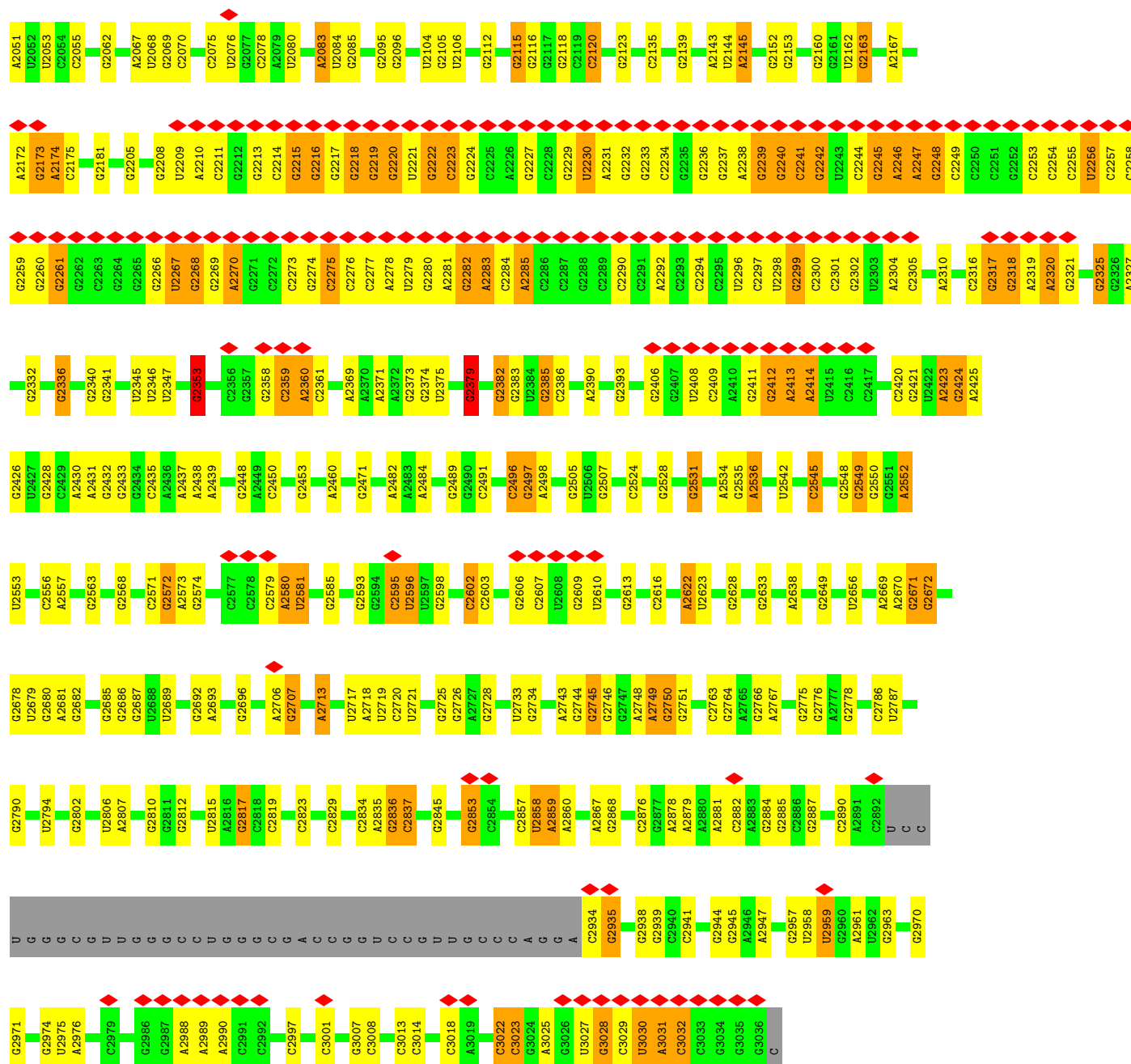
- Molecule 26: Predicted zinc-ribbon RNA-binding protein involved in translation



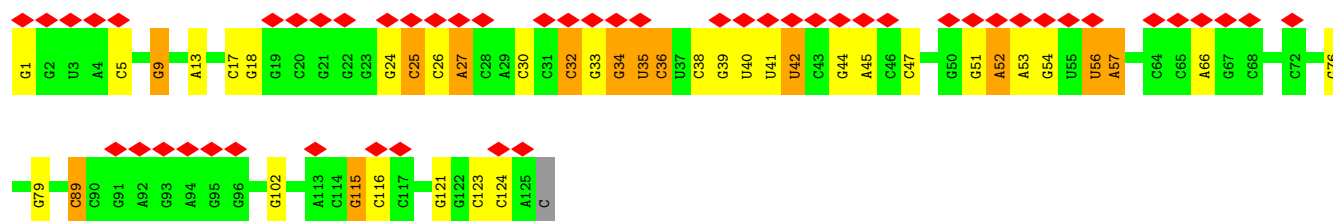
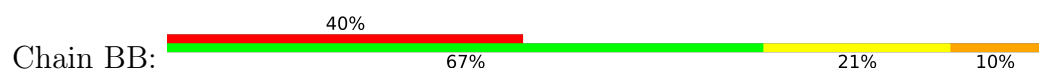
- Molecule 27: 23S ribosomal RNA





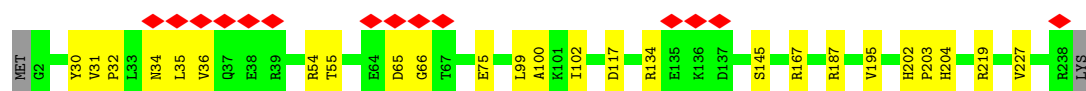


• Molecule 28: 5S ribosomal RNA



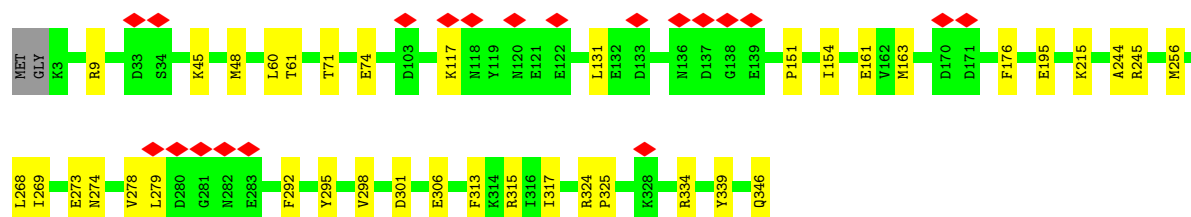
• Molecule 29: 50S ribosomal protein L2

Chain BC: 



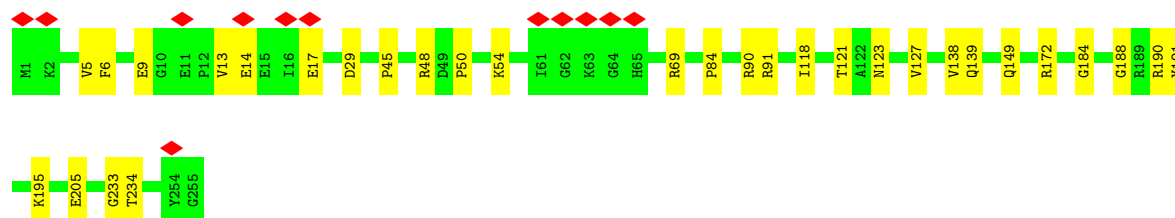
- Molecule 30: 50S ribosomal protein L3

Chain BD: 



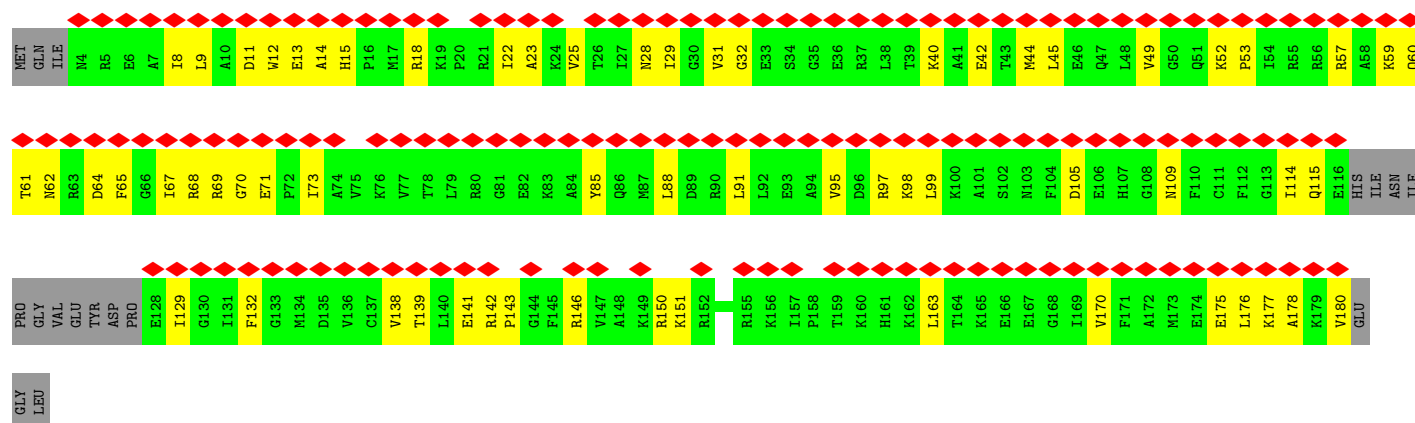
- Molecule 31: 50S ribosomal protein L4

Chain BE: 

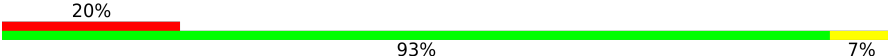


- Molecule 32: 50S ribosomal protein L5

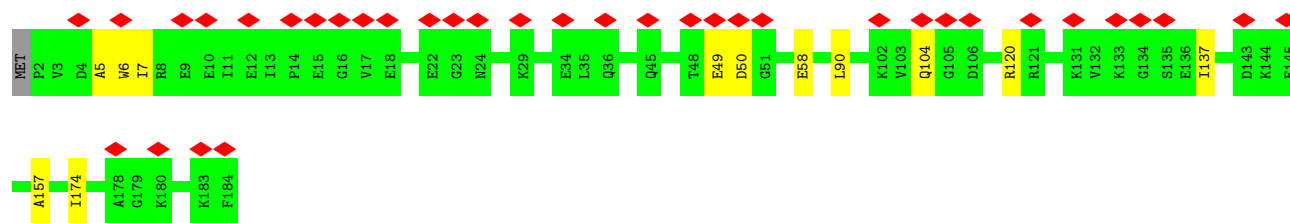
Chain BF: 



- Molecule 33: 50S ribosomal protein L6

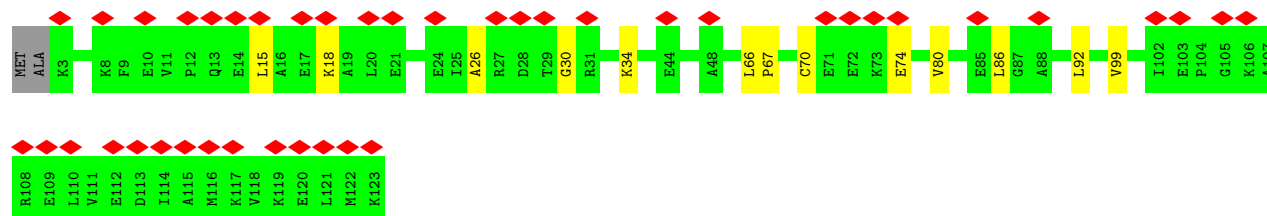
Chain BG: 





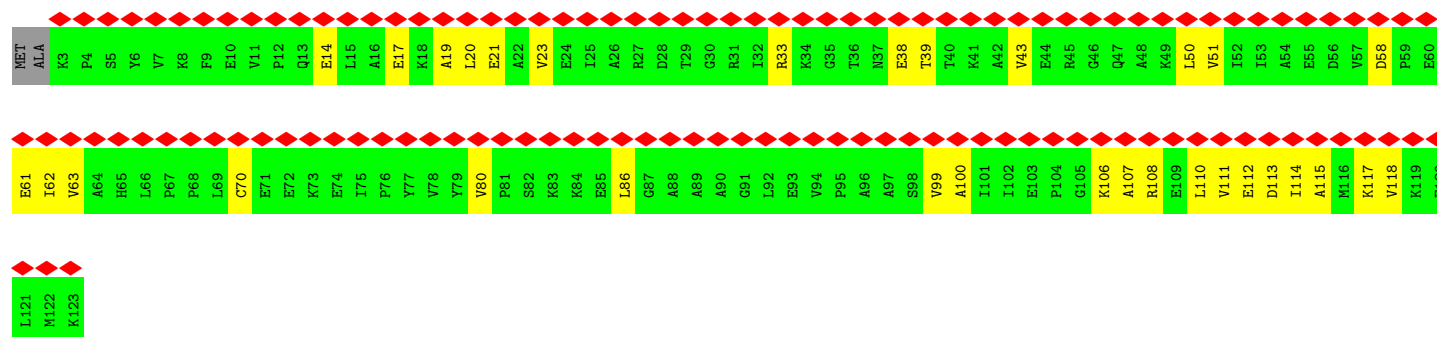
- Molecule 34: 50S ribosomal protein L7Ae

Chain BH: 34% 88% 11% .



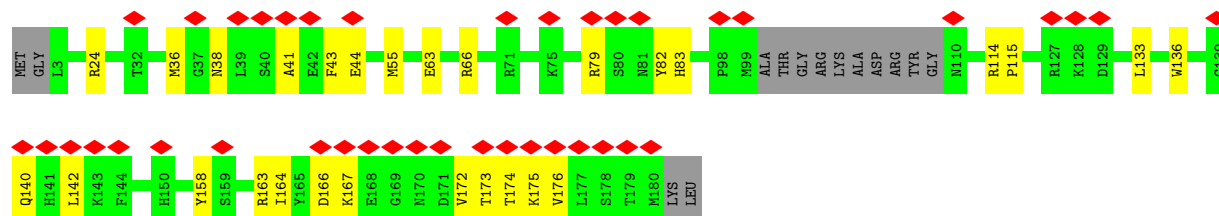
- Molecule 34: 50S ribosomal protein L7Ae

Chain BI: 98% 72% 26% .



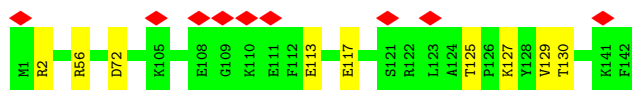
- Molecule 35: 50S ribosomal protein L10e

Chain BJ: 22% 77% 15% 8%



- Molecule 36: 50S ribosomal protein L13

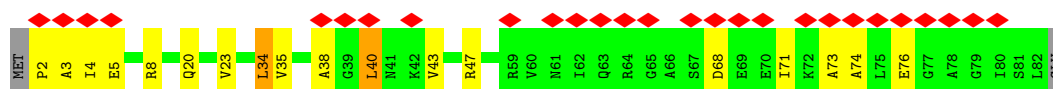
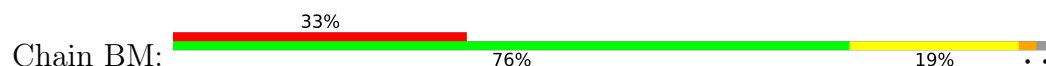
Chain BK: 6% 94% 6%



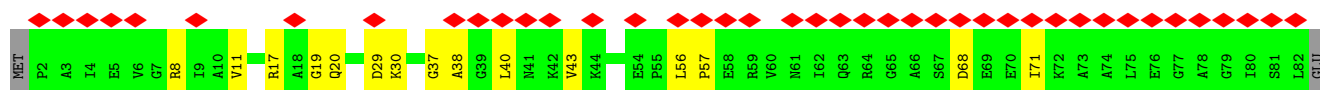
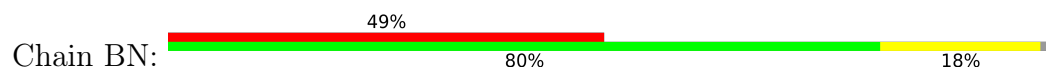
- Molecule 37: 50S ribosomal protein L14



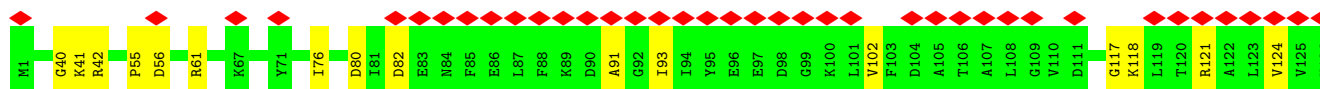
- Molecule 38: 50S ribosomal protein L14e



- Molecule 38: 50S ribosomal protein L14e



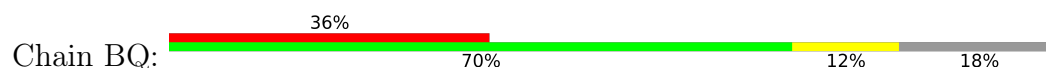
- Molecule 39: 50S ribosomal protein L15

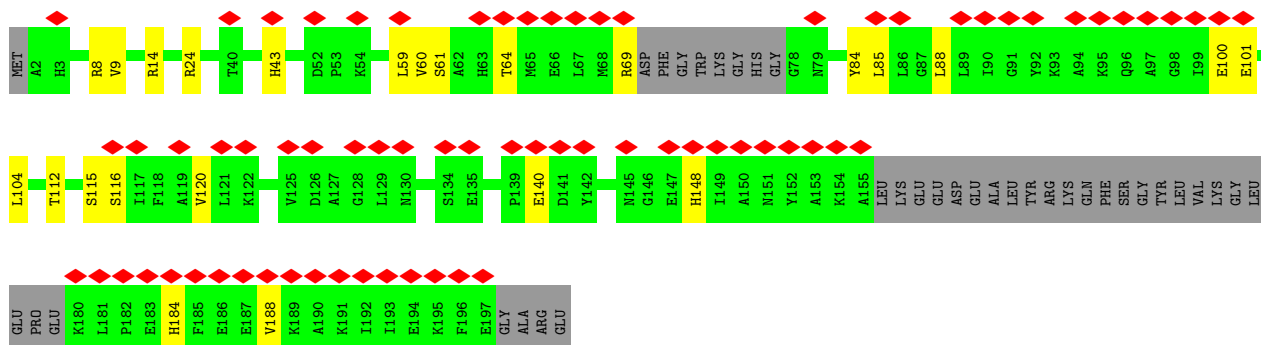


- Molecule 40: 50S ribosomal protein L15e



- Molecule 41: 50S ribosomal protein L18





- Molecule 42: 50S ribosomal protein L18e

Chain BR: 86% 13% .



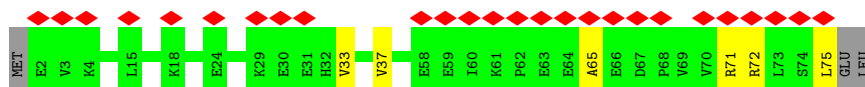
- Molecule 43: 50S ribosomal protein L19e

Chain BS: 85% 12% .



- Molecule 44: 50S ribosomal protein L18Ae

Chain BT: 34% 88% 8% .



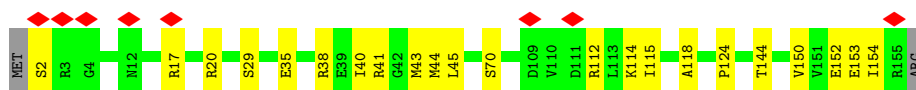
- Molecule 45: 50S ribosomal protein L21e

Chain BU: 89% 9% .

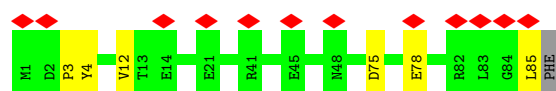


- Molecule 46: 50S ribosomal protein L22

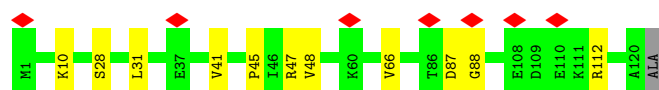
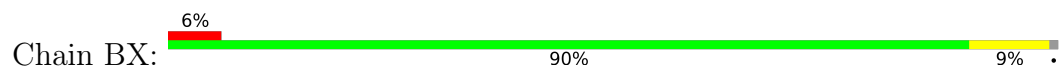
Chain BV: 5% 85% 14% .



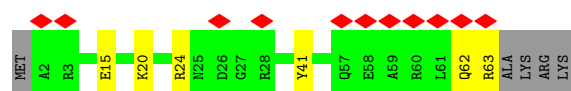
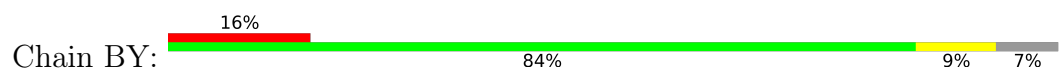
- Molecule 47: 50S ribosomal protein L23



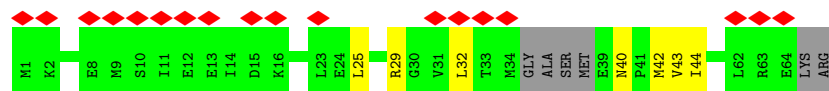
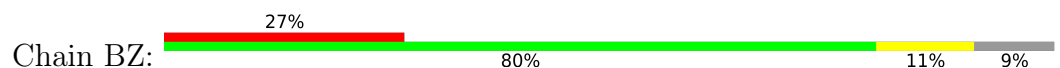
- Molecule 48: 50S ribosomal protein L24



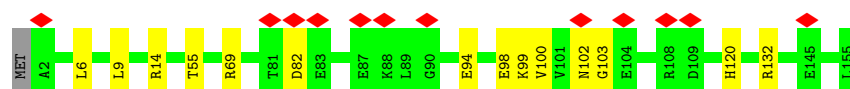
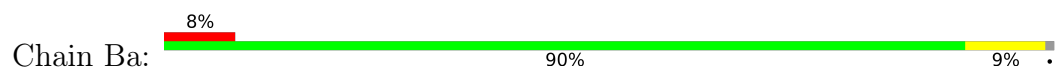
- Molecule 49: 50S ribosomal protein L24e



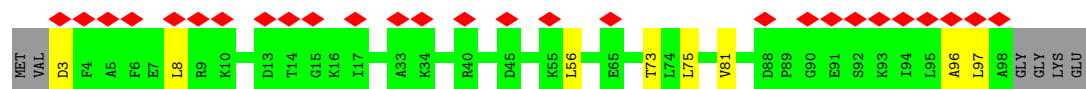
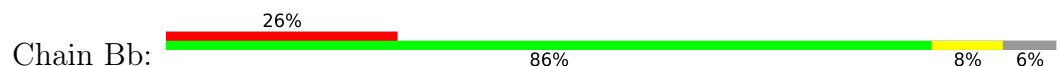
- Molecule 50: 50S ribosomal protein L29



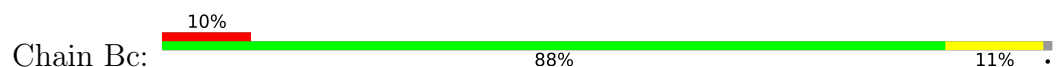
- Molecule 51: 50S ribosomal protein L30



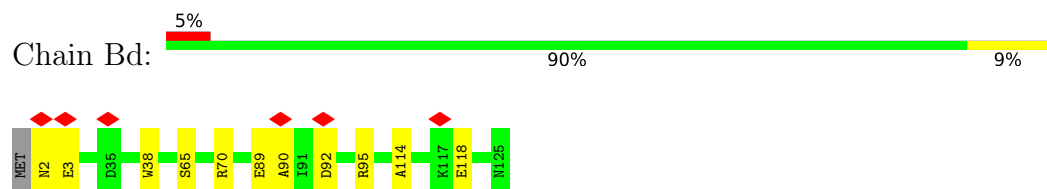
- Molecule 52: 50S ribosomal protein L30e



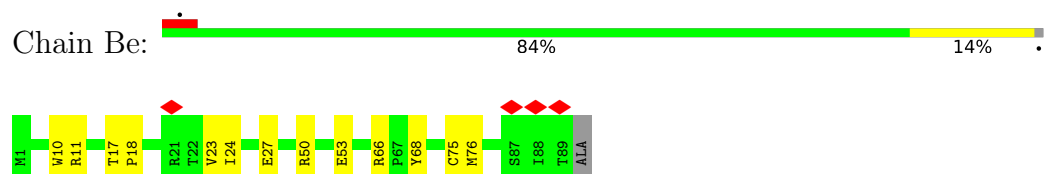
- Molecule 53: 50S ribosomal protein L31e



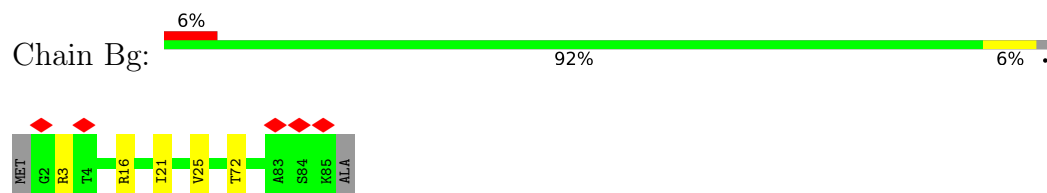
- Molecule 54: 50S ribosomal protein L32e



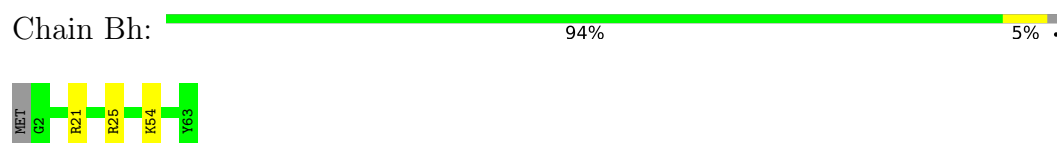
- Molecule 55: 50S ribosomal protein L34e



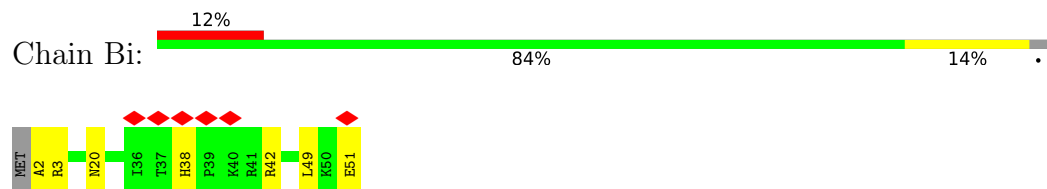
- Molecule 56: 50S ribosomal protein L37Ae



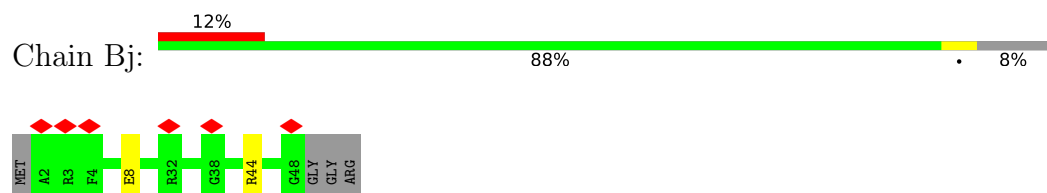
- Molecule 57: 50S ribosomal protein L37e



- Molecule 58: 50S ribosomal protein L39e



- Molecule 59: 50S ribosomal protein L40e

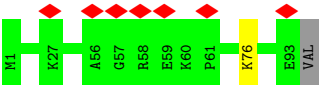


- Molecule 60: LSU ribosomal protein L41E





- Molecule 61: 50S ribosomal protein L44e



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	283424	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	29000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.506	Depositor
Minimum map value	-0.277	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, 4AC, 5MC, A2M, MA6, OMC, 6MZ, 4SU, 5MU, ZN, OMU, LV2, LHH

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	Aa	0.36	1/34630 (0.0%)	0.40	2/54028 (0.0%)
2	Ab	0.33	0/1611	0.42	0/2179
3	Ac	0.23	0/1534	0.38	0/2057
4	Ad	0.32	0/1578	0.45	0/2119
5	Ae	0.38	0/1477	0.46	0/1980
6	Af	0.43	0/1991	0.52	0/2688
7	Ag	0.43	0/1778	0.51	0/2393
8	Ah	0.29	0/968	0.44	0/1300
9	Ai	0.31	0/1738	0.43	0/2332
10	Aj	0.41	0/1039	0.49	0/1397
11	Ak	0.43	0/991	0.47	0/1322
12	Al	0.32	0/1068	0.44	0/1430
13	Am	0.25	0/810	0.42	0/1087
14	An	0.75	2/971 (0.2%)	0.85	3/1308 (0.2%)
15	Ao	0.40	0/1139	0.50	0/1518
16	Ap	0.31	0/1113	0.48	0/1500
17	Aq	0.43	0/1241	0.48	0/1667
18	Ar	0.30	0/457	0.48	0/602
19	As	0.40	0/888	0.46	0/1200
20	At	0.21	0/545	0.40	0/725
21	Au	0.30	0/970	0.36	0/1295
22	Av	0.34	0/1249	0.39	0/1687
23	Aw	0.34	0/790	0.45	0/1063
24	Ax	0.35	0/469	0.45	0/633
25	Ay	0.26	0/501	0.43	0/672
26	Az	0.35	0/440	0.44	0/599
27	BA	0.45	2/69303 (0.0%)	0.46	3/108170 (0.0%)
28	BB	0.26	0/2993	0.36	0/4668
29	BC	0.53	0/1860	0.73	2/2511 (0.1%)
30	BD	0.51	0/2815	0.63	0/3795
31	BE	0.47	0/2066	0.61	0/2785
32	BF	0.31	0/1355	0.59	0/1806

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BG	0.32	0/1490	0.48	0/2006
34	BH	0.35	0/941	0.45	0/1272
34	BI	0.25	0/941	0.51	0/1272
35	BJ	0.39	0/1407	0.51	0/1891
36	BK	0.46	0/1165	0.60	0/1558
37	BL	0.43	0/1067	0.56	0/1435
38	BM	0.53	0/614	0.71	0/824
38	BN	0.32	0/614	0.58	0/824
39	BO	0.43	0/1184	0.59	0/1581
40	BP	0.53	0/1621	0.63	0/2163
41	BQ	0.31	0/1342	0.48	0/1804
42	BR	0.45	0/971	0.54	0/1301
43	BS	0.46	0/1216	0.58	0/1607
44	BT	0.32	0/636	0.47	0/852
45	BU	0.45	0/806	0.54	0/1080
46	BV	0.45	0/1259	0.56	0/1688
47	BW	0.39	0/690	0.52	0/925
48	BX	0.48	0/1007	0.59	0/1344
49	BY	0.45	0/538	0.56	0/716
50	BZ	0.42	0/506	0.53	0/668
51	Ba	0.45	0/1259	0.54	0/1680
52	Bb	0.33	0/742	0.49	0/1001
53	Bc	0.45	0/736	0.54	0/990
54	Bd	0.46	0/1044	0.56	0/1394
55	Be	0.47	0/746	0.59	0/997
56	Bg	0.52	0/640	0.72	2/855 (0.2%)
57	Bh	0.64	0/524	0.66	0/692
58	Bi	0.53	0/441	0.63	0/588
59	Bj	0.35	0/381	0.52	0/505
60	Bk	0.78	0/351	0.82	0/454
61	Bl	0.45	0/796	0.51	0/1056
All	All	0.42	5/170053 (0.0%)	0.47	12/251539 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
14	An	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	An	125	PRO	N-CA	18.13	1.70	1.47
27	BA	849	A2M	O3'-P	5.20	1.61	1.56
1	Aa	352	A2M	O3'-P	5.18	1.61	1.56
27	BA	2553	4SU	O3'-P	5.05	1.61	1.56
14	An	124	ILE	C-N	5.02	1.45	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	An	124	ILE	CA-C-N	14.96	138.54	119.84
14	An	124	ILE	C-N-CA	14.96	138.54	119.84
14	An	125	PRO	CA-N-CD	-8.33	100.34	112.00
56	Bg	16	ARG	CA-C-N	6.17	133.32	121.54
56	Bg	16	ARG	C-N-CA	6.17	133.32	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	An	126	HIS	Peptide
14	An	127	ASP	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	31499	0	15927	225	0
2	Ab	1580	0	1634	14	0
3	Ac	1513	0	1598	9	0
4	Ad	1550	0	1618	11	0
5	Ae	1454	0	1521	6	0
6	Af	1945	0	2028	14	0
7	Ag	1753	0	1820	35	0
8	Ah	952	0	997	7	0
9	Ai	1706	0	1772	24	0
10	Aj	1020	0	1066	2	0
11	Ak	982	0	1071	8	0
12	Al	1054	0	1105	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	Am	803	0	854	9	0
14	An	953	0	973	9	0
15	Ao	1122	0	1212	8	0
16	Ap	1090	0	1121	19	0
17	Aq	1217	0	1302	13	0
18	Ar	447	0	469	7	0
19	As	868	0	895	7	0
20	At	538	0	560	8	0
21	Au	952	0	1000	8	0
22	Av	1216	0	1236	12	0
23	Aw	777	0	797	6	0
24	Ax	461	0	494	2	0
25	Ay	499	0	528	8	0
26	Az	426	0	403	2	0
27	BA	63188	0	31965	598	0
28	BB	2678	0	1361	25	0
29	BC	1820	0	1902	18	0
30	BD	2746	0	2840	28	0
31	BE	2026	0	2128	19	0
32	BF	1338	0	1403	50	0
33	BG	1463	0	1520	9	0
34	BH	928	0	970	7	0
34	BI	928	0	970	23	0
35	BJ	1378	0	1409	23	0
36	BK	1146	0	1213	6	0
37	BL	1055	0	1134	5	0
38	BM	610	0	660	20	0
38	BN	610	0	660	10	0
39	BO	1162	0	1218	11	0
40	BP	1582	0	1677	8	0
41	BQ	1314	0	1359	20	0
42	BR	959	0	1018	9	0
43	BS	1200	0	1298	15	0
44	BT	624	0	647	3	0
45	BU	784	0	821	7	0
46	BV	1234	0	1274	16	0
47	BW	683	0	743	4	0
48	BX	991	0	1053	8	0
49	BY	524	0	512	5	0
50	BZ	506	0	559	4	0
51	Ba	1242	0	1332	11	0
52	Bb	730	0	768	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Bc	721	0	776	6	0
54	Bd	1022	0	1106	7	0
55	Be	728	0	785	10	0
56	Bg	630	0	675	3	0
57	Bh	512	0	527	4	0
58	Bi	432	0	488	6	0
59	Bj	373	0	391	1	0
60	Bk	345	0	407	3	0
61	Bl	778	0	833	1	0
62	Ag	1	0	0	0	0
62	Ar	1	0	0	0	0
62	As	1	0	0	0	0
62	Ax	1	0	0	0	0
62	Az	2	0	0	0	0
62	BY	1	0	0	0	0
62	Be	1	0	0	0	0
62	Bg	1	0	0	0	0
62	Bh	1	0	0	0	0
62	Bj	1	0	0	0	0
62	Bl	1	0	0	0	0
63	Aa	153	0	0	43	0
63	Ae	1	0	0	0	0
63	Af	5	0	0	0	0
63	Ag	1	0	0	0	0
63	Ai	1	0	0	0	0
63	Aj	1	0	0	0	0
63	Ak	2	0	0	0	0
63	Al	2	0	0	0	0
63	An	1	0	0	0	0
63	Ao	2	0	0	1	0
63	Ap	1	0	0	0	0
63	Aq	5	0	0	1	0
63	Av	1	0	0	0	0
63	Az	1	0	0	0	0
63	BA	1674	0	0	279	0
63	BB	7	0	0	1	0
63	BC	29	0	0	3	0
63	BD	30	0	0	0	0
63	BE	24	0	0	1	0
63	BF	1	0	0	0	0
63	BH	1	0	0	0	0
63	BJ	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	BK	7	0	0	1	0
63	BL	8	0	0	1	0
63	BN	1	0	0	1	0
63	BO	19	0	0	0	0
63	BP	23	0	0	3	0
63	BQ	5	0	0	0	0
63	BR	1	0	0	0	0
63	BS	12	0	0	1	0
63	BV	17	0	0	5	0
63	BW	3	0	0	0	0
63	BX	7	0	0	1	0
63	BY	5	0	0	0	0
63	BZ	3	0	0	0	0
63	Ba	6	0	0	1	0
63	Bb	1	0	0	0	0
63	Bc	7	0	0	0	0
63	Bd	12	0	0	0	0
63	Be	7	0	0	1	0
63	Bg	6	0	0	1	0
63	Bh	18	0	0	0	0
63	Bi	5	0	0	1	0
63	Bk	6	0	0	0	0
63	Bl	3	0	0	0	0
All	All	161508	0	114403	1368	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1368 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Ag:75:ASP:OD1	7:Ag:77:GLY:CA	1.65	1.40
14:An:125:PRO:N	14:An:125:PRO:CA	1.70	1.39
7:Ag:75:ASP:CG	7:Ag:77:GLY:H	1.35	1.31
1:Aa:989:G:O6	1:Aa:1163:G:N7	1.59	1.31
1:Aa:1350:A:H61	7:Ag:75:ASP:CB	1.53	1.21

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ab	194/201 (96%)	175 (90%)	19 (10%)	0	100	100
3	Ac	187/209 (90%)	173 (92%)	14 (8%)	0	100	100
4	Ad	188/200 (94%)	176 (94%)	12 (6%)	0	100	100
5	Ae	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
6	Af	239/243 (98%)	229 (96%)	10 (4%)	0	100	100
7	Ag	219/235 (93%)	197 (90%)	22 (10%)	0	100	100
8	Ah	121/125 (97%)	113 (93%)	8 (7%)	0	100	100
9	Ai	209/215 (97%)	197 (94%)	12 (6%)	0	100	100
10	Aj	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
11	Ak	123/130 (95%)	111 (90%)	12 (10%)	0	100	100
12	Al	131/135 (97%)	124 (95%)	7 (5%)	0	100	100
13	Am	98/102 (96%)	90 (92%)	8 (8%)	0	100	100
14	An	125/140 (89%)	114 (91%)	11 (9%)	0	100	100
15	Ao	141/147 (96%)	134 (95%)	7 (5%)	0	100	100
16	Ap	133/149 (89%)	114 (86%)	19 (14%)	0	100	100
17	Aq	147/151 (97%)	135 (92%)	12 (8%)	0	100	100
18	Ar	52/56 (93%)	45 (86%)	7 (14%)	0	100	100
19	As	105/114 (92%)	98 (93%)	7 (7%)	0	100	100
20	At	62/67 (92%)	56 (90%)	6 (10%)	0	100	100
21	Au	114/133 (86%)	107 (94%)	7 (6%)	0	100	100
22	Av	147/150 (98%)	143 (97%)	4 (3%)	0	100	100
23	Aw	93/98 (95%)	87 (94%)	6 (6%)	0	100	100
24	Ax	59/65 (91%)	51 (86%)	8 (14%)	0	100	100
25	Ay	62/70 (89%)	56 (90%)	6 (10%)	0	100	100
26	Az	53/62 (86%)	47 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	BC	235/239 (98%)	216 (92%)	19 (8%)	0	100	100
30	BD	342/346 (99%)	325 (95%)	17 (5%)	0	100	100
31	BE	253/255 (99%)	242 (96%)	11 (4%)	0	100	100
32	BF	162/183 (88%)	122 (75%)	40 (25%)	0	100	100
33	BG	181/184 (98%)	163 (90%)	18 (10%)	0	100	100
34	BH	119/123 (97%)	110 (92%)	9 (8%)	0	100	100
34	BI	119/123 (97%)	105 (88%)	14 (12%)	0	100	100
35	BJ	164/182 (90%)	147 (90%)	17 (10%)	0	100	100
36	BK	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
37	BL	138/141 (98%)	132 (96%)	6 (4%)	0	100	100
38	BM	79/83 (95%)	65 (82%)	14 (18%)	0	100	100
38	BN	79/83 (95%)	61 (77%)	18 (23%)	0	100	100
39	BO	146/148 (99%)	130 (89%)	16 (11%)	0	100	100
40	BP	191/194 (98%)	184 (96%)	7 (4%)	0	100	100
41	BQ	158/201 (79%)	142 (90%)	16 (10%)	0	100	100
42	BR	118/121 (98%)	113 (96%)	5 (4%)	0	100	100
43	BS	144/150 (96%)	140 (97%)	4 (3%)	0	100	100
44	BT	72/77 (94%)	67 (93%)	5 (7%)	0	100	100
45	BU	94/98 (96%)	91 (97%)	3 (3%)	0	100	100
46	BV	152/156 (97%)	145 (95%)	7 (5%)	0	100	100
47	BW	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
48	BX	118/121 (98%)	113 (96%)	5 (4%)	0	100	100
49	BY	60/67 (90%)	60 (100%)	0	0	100	100
50	BZ	56/66 (85%)	52 (93%)	4 (7%)	0	100	100
51	Ba	152/155 (98%)	140 (92%)	12 (8%)	0	100	100
52	Bb	94/102 (92%)	84 (89%)	10 (11%)	0	100	100
53	Bc	87/90 (97%)	80 (92%)	7 (8%)	0	100	100
54	Bd	122/125 (98%)	119 (98%)	3 (2%)	0	100	100
55	Be	87/90 (97%)	77 (88%)	10 (12%)	0	100	100
56	Bg	82/86 (95%)	76 (93%)	6 (7%)	0	100	100
57	Bh	60/63 (95%)	57 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	Bi	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
59	Bj	45/51 (88%)	41 (91%)	4 (9%)	0	100	100
60	Bk	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
61	Bl	91/94 (97%)	91 (100%)	0	0	100	100
All	All	7606/8020 (95%)	7033 (92%)	573 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ab	170/175 (97%)	170 (100%)	0	100	100
3	Ac	155/168 (92%)	155 (100%)	0	100	100
4	Ad	162/169 (96%)	162 (100%)	0	100	100
5	Ae	153/156 (98%)	153 (100%)	0	100	100
6	Af	210/212 (99%)	210 (100%)	0	100	100
7	Ag	185/197 (94%)	185 (100%)	0	100	100
8	Ah	104/105 (99%)	104 (100%)	0	100	100
9	Ai	182/184 (99%)	182 (100%)	0	100	100
10	Aj	106/107 (99%)	106 (100%)	0	100	100
11	Ak	101/105 (96%)	101 (100%)	0	100	100
12	Al	110/112 (98%)	110 (100%)	0	100	100
13	Am	89/91 (98%)	89 (100%)	0	100	100
14	An	95/108 (88%)	95 (100%)	0	100	100
15	Ao	117/120 (98%)	117 (100%)	0	100	100
16	Ap	111/123 (90%)	111 (100%)	0	100	100
17	Aq	129/131 (98%)	129 (100%)	0	100	100
18	Ar	45/46 (98%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	As	95/101 (94%)	95 (100%)	0	100	100
20	At	58/61 (95%)	58 (100%)	0	100	100
21	Au	104/117 (89%)	104 (100%)	0	100	100
22	Av	125/126 (99%)	125 (100%)	0	100	100
23	Aw	85/88 (97%)	85 (100%)	0	100	100
24	Ax	53/56 (95%)	53 (100%)	0	100	100
25	Ay	53/59 (90%)	53 (100%)	0	100	100
26	Az	49/55 (89%)	49 (100%)	0	100	100
29	BC	185/187 (99%)	185 (100%)	0	100	100
30	BD	288/289 (100%)	288 (100%)	0	100	100
31	BE	212/212 (100%)	212 (100%)	0	100	100
32	BF	140/155 (90%)	140 (100%)	0	100	100
33	BG	158/159 (99%)	158 (100%)	0	100	100
34	BH	99/100 (99%)	99 (100%)	0	100	100
34	BI	99/100 (99%)	99 (100%)	0	100	100
35	BJ	144/153 (94%)	144 (100%)	0	100	100
36	BK	120/120 (100%)	120 (100%)	0	100	100
37	BL	104/105 (99%)	104 (100%)	0	100	100
38	BM	63/65 (97%)	61 (97%)	2 (3%)	34	51
38	BN	63/65 (97%)	63 (100%)	0	100	100
39	BO	115/116 (99%)	115 (100%)	0	100	100
40	BP	161/162 (99%)	161 (100%)	0	100	100
41	BQ	138/167 (83%)	138 (100%)	0	100	100
42	BR	101/102 (99%)	101 (100%)	0	100	100
43	BS	120/124 (97%)	120 (100%)	0	100	100
44	BT	69/72 (96%)	69 (100%)	0	100	100
45	BU	84/85 (99%)	84 (100%)	0	100	100
46	BV	129/131 (98%)	129 (100%)	0	100	100
47	BW	75/76 (99%)	75 (100%)	0	100	100
48	BX	109/109 (100%)	109 (100%)	0	100	100
49	BY	54/58 (93%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	BZ	57/61 (93%)	57 (100%)	0	100	100
51	Ba	132/133 (99%)	132 (100%)	0	100	100
52	Bb	76/80 (95%)	76 (100%)	0	100	100
53	Bc	75/76 (99%)	75 (100%)	0	100	100
54	Bd	106/107 (99%)	106 (100%)	0	100	100
55	Be	80/80 (100%)	80 (100%)	0	100	100
56	Bg	62/63 (98%)	62 (100%)	0	100	100
57	Bh	50/51 (98%)	50 (100%)	0	100	100
58	Bi	45/46 (98%)	45 (100%)	0	100	100
59	Bj	36/38 (95%)	36 (100%)	0	100	100
60	Bk	34/35 (97%)	34 (100%)	0	100	100
61	Bl	83/84 (99%)	83 (100%)	0	100	100
All	All	6512/6738 (97%)	6510 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BM	34	LEU
38	BM	40	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
35	BJ	110	ASN
42	BR	44	GLN
35	BJ	150	HIS
40	BP	115	ASN
45	BU	33	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Aa	1457/1498 (97%)	237 (16%)	0
27	BA	2929/3037 (96%)	526 (17%)	36 (1%)
28	BB	124/126 (98%)	22 (17%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4510/4661 (96%)	785 (17%)	37 (0%)

5 of 785 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Aa	4	C
1	Aa	5	4AC
1	Aa	17	C
1	Aa	33	U
1	Aa	35	G

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	BA	2496	C
27	BA	3022	C
27	BA	2534	A
27	BA	2836	G
27	BA	1182	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

81 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	A2M	BA	932	27	22,25,26	3.38	10 (45%)	31,36,39	2.47	9 (29%)
27	OMU	BA	1949	27	19,22,23	2.85	7 (36%)	26,31,34	1.66	5 (19%)
27	A2M	BA	879	27	22,25,26	3.35	10 (45%)	31,36,39	2.48	9 (29%)
27	OMU	BA	657	27	19,22,23	2.80	7 (36%)	26,31,34	1.67	4 (15%)
27	OMG	BA	1953	27	23,26,27	2.16	7 (30%)	33,38,41	1.69	8 (24%)
1	MA6	Aa	1468	1	23,26,27	1.46	4 (17%)	34,38,41	3.24	10 (29%)
1	OMU	Aa	8	1	19,22,23	2.82	7 (36%)	26,31,34	1.80	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	OMG	BA	65	27	23,26,27	2.20	7 (30%)	33,38,41	1.61	8 (24%)
27	OMG	BA	912	27	23,26,27	2.21	7 (30%)	33,38,41	1.90	8 (24%)
27	OMG	BA	2010	27	23,26,27	2.21	7 (30%)	33,38,41	1.62	7 (21%)
1	OMG	Aa	446	1	23,26,27	2.21	7 (30%)	33,38,41	1.64	7 (21%)
27	OMG	BA	800	27	23,26,27	2.15	7 (30%)	33,38,41	1.59	7 (21%)
1	OMC	Aa	1354	1	19,22,23	2.82	8 (42%)	26,31,34	0.81	0
27	OMC	BA	2047	27	19,22,23	2.69	7 (36%)	26,31,34	0.88	0
1	4AC	Aa	5	1	21,24,25	3.15	10 (47%)	29,34,37	0.93	2 (6%)
27	OMG	BA	668	27	23,26,27	2.21	7 (30%)	33,38,41	1.60	7 (21%)
27	OMG	BA	2550	27	23,26,27	2.22	7 (30%)	33,38,41	1.60	7 (21%)
27	OMC	BA	1721	27	19,22,23	2.71	7 (36%)	26,31,34	0.97	0
27	OMC	BA	1820	27	19,22,23	2.70	7 (36%)	26,31,34	0.99	2 (7%)
27	OMC	BA	1709	27	19,22,23	2.82	7 (36%)	26,31,34	0.83	0
27	OMU	BA	1776	27	19,22,23	2.86	7 (36%)	26,31,34	1.62	6 (23%)
1	OMG	Aa	529	1	23,26,27	2.17	7 (30%)	33,38,41	1.59	6 (18%)
1	LV2	Aa	918	1	20,23,24	0.91	0	26,33,36	0.77	0
1	5MC	Aa	672	1	18,22,23	3.25	7 (38%)	26,32,35	1.00	2 (7%)
27	OMG	BA	2672	27	23,26,27	2.23	7 (30%)	33,38,41	1.76	7 (21%)
27	OMG	BA	63	27	23,26,27	2.24	8 (34%)	33,38,41	1.68	8 (24%)
27	OMG	BA	2379	27	23,26,27	2.15	7 (30%)	33,38,41	1.58	6 (18%)
1	OMG	Aa	659	1	23,26,27	2.25	8 (34%)	33,38,41	1.73	8 (24%)
27	OMG	BA	215	27	23,26,27	2.27	8 (34%)	33,38,41	1.67	7 (21%)
27	OMC	BA	477	27	19,22,23	2.88	7 (36%)	26,31,34	0.97	1 (3%)
27	OMG	BA	491	27	23,26,27	2.14	7 (30%)	33,38,41	1.66	8 (24%)
1	OMG	Aa	852	1	23,26,27	2.19	7 (30%)	33,38,41	1.68	7 (21%)
27	OMG	BA	1129	27	23,26,27	2.20	8 (34%)	33,38,41	1.63	7 (21%)
27	OMU	BA	1969	27	19,22,23	2.91	7 (36%)	26,31,34	1.78	6 (23%)
27	OMC	BA	2876	27	19,22,23	2.72	7 (36%)	26,31,34	1.00	0
27	A2M	BA	2145	27	22,25,26	3.44	10 (45%)	31,36,39	2.47	10 (32%)
27	OMG	BA	674	27	23,26,27	2.17	7 (30%)	33,38,41	1.56	6 (18%)
1	MA6	Aa	1467	1	23,26,27	1.37	3 (13%)	34,38,41	3.07	11 (32%)
27	OMG	BA	2613	27	23,26,27	2.16	8 (34%)	33,38,41	1.62	6 (18%)
27	OMU	BA	1623	27	19,22,23	2.85	8 (42%)	26,31,34	1.65	5 (19%)
27	OMC	BA	2545	27	19,22,23	2.70	7 (36%)	26,31,34	0.81	1 (3%)
27	OMU	BA	1905	27	19,22,23	2.76	8 (42%)	26,31,34	1.55	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	Aa	498	1	23,26,27	2.19	8 (34%)	33,38,41	1.63	7 (21%)
27	A2M	BA	61	27	22,25,26	3.39	10 (45%)	31,36,39	2.53	11 (35%)
1	4AC	Aa	458	1	21,24,25	1.07	1 (4%)	29,34,37	1.13	3 (10%)
27	OMG	BA	2016	27	23,26,27	2.23	7 (30%)	33,38,41	1.59	6 (18%)
1	5MC	Aa	1352	1	18,22,23	3.43	7 (38%)	26,32,35	1.00	2 (7%)
1	5MU	Aa	917	1	19,22,23	1.40	5 (26%)	28,32,35	2.18	6 (21%)
27	5MC	BA	1965	27	18,22,23	3.31	7 (38%)	26,32,35	0.95	3 (11%)
27	OMU	BA	2656	27	19,22,23	2.91	7 (36%)	26,31,34	1.71	5 (19%)
27	OMG	BA	2353	27	23,26,27	2.37	8 (34%)	33,38,41	1.88	8 (24%)
27	OMG	BA	2745	27	23,26,27	2.20	7 (30%)	33,38,41	1.61	7 (21%)
27	OMG	BA	833	27	23,26,27	2.21	7 (30%)	33,38,41	1.64	7 (21%)
27	OMG	BA	943	27	23,26,27	2.20	7 (30%)	33,38,41	1.94	10 (30%)
27	A2M	BA	1109	27	22,25,26	3.34	10 (45%)	31,36,39	2.58	10 (32%)
1	A2M	Aa	352	1	22,25,26	3.41	9 (40%)	31,36,39	2.46	10 (32%)
1	4AC	Aa	730	1	21,24,25	3.21	10 (47%)	29,34,37	0.96	2 (6%)
1	OMG	Aa	450	1	23,26,27	1.24	3 (13%)	33,38,41	1.98	7 (21%)
1	OMG	Aa	913	1	23,26,27	2.28	9 (39%)	33,38,41	1.77	7 (21%)
27	A2M	BA	849	27	22,25,26	3.35	9 (40%)	31,36,39	2.47	9 (29%)
27	OMG	BA	2115	27	23,26,27	2.16	7 (30%)	33,38,41	1.47	6 (18%)
27	OMU	BA	2542	27	19,22,23	2.86	7 (36%)	26,31,34	1.60	5 (19%)
27	4SU	BA	2553	27	18,21,22	4.08	8 (44%)	26,30,33	1.94	5 (19%)
1	5MC	Aa	854	1	18,22,23	0.96	2 (11%)	26,32,35	1.27	3 (11%)
27	LHH	BA	501	27	22,25,26	2.41	4 (18%)	29,35,38	1.23	4 (13%)
27	OMG	BA	2528	27	23,26,27	2.28	8 (34%)	33,38,41	1.63	7 (21%)
1	OMG	Aa	548	1	23,26,27	2.24	8 (34%)	33,38,41	1.72	7 (21%)
1	6MZ	Aa	1449	1	22,25,26	1.42	4 (18%)	30,36,39	2.09	10 (33%)
27	5MC	BA	2075	27	18,22,23	3.27	7 (38%)	26,32,35	0.94	0
27	A2M	BA	872	27	22,25,26	3.35	10 (45%)	31,36,39	2.38	9 (29%)
27	OMU	BA	453	27	19,22,23	2.90	7 (36%)	26,31,34	1.71	5 (19%)
27	OMC	BA	2786	27	19,22,23	2.63	7 (36%)	26,31,34	0.93	1 (3%)
27	5MC	BA	342	27	18,22,23	3.37	7 (38%)	26,32,35	0.98	2 (7%)
1	4AC	Aa	1459	1	21,24,25	3.00	11 (52%)	29,34,37	1.08	3 (10%)
27	5MC	BA	875	27	18,22,23	3.33	7 (38%)	26,32,35	1.22	6 (23%)
27	A2M	BA	505	27	22,25,26	3.45	10 (45%)	31,36,39	2.60	11 (35%)
1	OMG	Aa	658	1	23,26,27	2.21	7 (30%)	33,38,41	1.82	9 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	OMG	BA	1945	27	23,26,27	2.15	7 (30%)	33,38,41	1.77	7 (21%)
27	5MC	BA	2055	27	18,22,23	3.41	7 (38%)	26,32,35	1.23	4 (15%)
27	OMC	BA	869	27	19,22,23	2.62	7 (36%)	26,31,34	1.06	2 (7%)
27	5MC	BA	2120	27	18,22,23	3.07	7 (38%)	26,32,35	1.28	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	A2M	BA	932	27	-	0/9/27/28	0/3/3/3
27	OMU	BA	1949	27	-	0/9/27/28	0/2/2/2
27	A2M	BA	879	27	-	0/9/27/28	0/3/3/3
27	OMU	BA	657	27	-	0/9/27/28	0/2/2/2
27	OMG	BA	1953	27	-	1/9/27/28	0/3/3/3
1	MA6	Aa	1468	1	-	1/11/29/30	0/3/3/3
1	OMU	Aa	8	1	-	3/9/27/28	0/2/2/2
27	OMG	BA	65	27	-	2/9/27/28	0/3/3/3
27	OMG	BA	912	27	-	0/9/27/28	0/3/3/3
27	OMG	BA	2010	27	-	0/9/27/28	0/3/3/3
1	OMG	Aa	446	1	-	1/9/27/28	0/3/3/3
27	OMG	BA	800	27	-	1/9/27/28	0/3/3/3
1	OMC	Aa	1354	1	-	0/9/27/28	0/2/2/2
27	OMC	BA	2047	27	-	0/9/27/28	0/2/2/2
1	4AC	Aa	5	1	-	2/11/29/30	0/2/2/2
27	OMG	BA	668	27	-	1/9/27/28	0/3/3/3
27	OMG	BA	2550	27	-	0/9/27/28	0/3/3/3
27	OMC	BA	1721	27	-	0/9/27/28	0/2/2/2
27	OMC	BA	1820	27	-	0/9/27/28	0/2/2/2
27	OMC	BA	1709	27	-	0/9/27/28	0/2/2/2
27	OMU	BA	1776	27	-	0/9/27/28	0/2/2/2
1	OMG	Aa	529	1	-	0/9/27/28	0/3/3/3
1	LV2	Aa	918	1	-	2/9/29/30	0/2/2/2
1	5MC	Aa	672	1	-	0/7/25/26	0/2/2/2
27	OMG	BA	2672	27	-	2/9/27/28	0/3/3/3
27	OMG	BA	63	27	-	0/9/27/28	0/3/3/3
27	OMG	BA	2379	27	-	3/9/27/28	0/3/3/3
1	OMG	Aa	659	1	-	2/9/27/28	0/3/3/3
27	OMG	BA	215	27	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	OMC	BA	477	27	-	0/9/27/28	0/2/2/2
27	OMG	BA	491	27	-	1/9/27/28	0/3/3/3
1	OMG	Aa	852	1	-	1/9/27/28	0/3/3/3
27	OMG	BA	1129	27	-	0/9/27/28	0/3/3/3
27	OMU	BA	1969	27	-	0/9/27/28	0/2/2/2
27	OMC	BA	2876	27	-	0/9/27/28	0/2/2/2
27	A2M	BA	2145	27	-	0/9/27/28	0/3/3/3
27	OMG	BA	674	27	-	2/9/27/28	0/3/3/3
1	MA6	Aa	1467	1	-	0/11/29/30	0/3/3/3
27	OMG	BA	2613	27	-	0/9/27/28	0/3/3/3
27	OMU	BA	1623	27	-	2/9/27/28	0/2/2/2
27	OMC	BA	2545	27	-	1/9/27/28	0/2/2/2
27	OMU	BA	1905	27	-	0/9/27/28	0/2/2/2
1	OMG	Aa	498	1	-	0/9/27/28	0/3/3/3
27	A2M	BA	61	27	-	2/9/27/28	0/3/3/3
1	4AC	Aa	458	1	-	3/11/29/30	0/2/2/2
27	OMG	BA	2016	27	-	0/9/27/28	0/3/3/3
1	5MC	Aa	1352	1	-	0/7/25/26	0/2/2/2
1	5MU	Aa	917	1	-	0/7/25/26	0/2/2/2
27	5MC	BA	1965	27	-	0/7/25/26	0/2/2/2
27	OMU	BA	2656	27	-	0/9/27/28	0/2/2/2
27	OMG	BA	2353	27	-	2/9/27/28	0/3/3/3
27	OMG	BA	2745	27	-	0/9/27/28	0/3/3/3
27	OMG	BA	833	27	-	0/9/27/28	0/3/3/3
27	OMG	BA	943	27	-	0/9/27/28	0/3/3/3
27	A2M	BA	1109	27	-	0/9/27/28	0/3/3/3
1	A2M	Aa	352	1	-	0/9/27/28	0/3/3/3
1	4AC	Aa	730	1	-	0/11/29/30	0/2/2/2
1	OMG	Aa	450	1	-	0/9/27/28	0/3/3/3
1	OMG	Aa	913	1	-	2/9/27/28	0/3/3/3
27	A2M	BA	849	27	-	2/9/27/28	0/3/3/3
27	OMG	BA	2115	27	-	1/9/27/28	0/3/3/3
27	OMU	BA	2542	27	-	0/9/27/28	0/2/2/2
27	4SU	BA	2553	27	-	0/7/25/26	0/2/2/2
1	5MC	Aa	854	1	-	0/7/25/26	0/2/2/2
27	LHH	BA	501	27	-	0/13/31/32	0/2/2/2
27	OMG	BA	2528	27	-	0/9/27/28	0/3/3/3
1	OMG	Aa	548	1	-	0/9/27/28	0/3/3/3
1	6MZ	Aa	1449	1	-	0/9/27/28	0/3/3/3
27	5MC	BA	2075	27	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	A2M	BA	872	27	-	0/9/27/28	0/3/3/3
27	OMU	BA	453	27	-	0/9/27/28	0/2/2/2
27	OMC	BA	2786	27	-	2/9/27/28	0/2/2/2
27	5MC	BA	342	27	-	2/7/25/26	0/2/2/2
1	4AC	Aa	1459	1	-	0/11/29/30	0/2/2/2
27	5MC	BA	875	27	-	2/7/25/26	0/2/2/2
27	A2M	BA	505	27	-	2/9/27/28	0/3/3/3
1	OMG	Aa	658	1	-	0/9/27/28	0/3/3/3
27	OMG	BA	1945	27	-	2/9/27/28	0/3/3/3
27	5MC	BA	2055	27	-	0/7/25/26	0/2/2/2
27	OMC	BA	869	27	-	2/9/27/28	0/2/2/2
27	5MC	BA	2120	27	-	0/7/25/26	0/2/2/2

The worst 5 of 580 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	BA	2553	4SU	C2'-N1	8.76	1.52	1.38
27	BA	879	A2M	C2'-C1'	-8.54	1.31	1.53
1	Aa	352	A2M	C2'-C1'	-8.54	1.31	1.53
27	BA	61	A2M	C2'-C1'	-8.50	1.31	1.53
27	BA	1965	5MC	C6-C5	8.50	1.48	1.34

The worst 5 of 457 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Aa	1468	MA6	N1-C6-N6	-13.07	102.80	117.08
1	Aa	1467	MA6	N1-C6-N6	-12.09	103.87	117.08
1	Aa	1468	MA6	C5-C6-N6	6.64	136.87	125.30
27	BA	1109	A2M	N6-C6-N1	-6.63	103.83	118.35
27	BA	2553	4SU	C4-N3-C2	-6.62	120.91	127.34

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	Aa	5	4AC	O4'-C4'-C5'-O5'
1	Aa	5	4AC	C3'-C4'-C5'-O5'
1	Aa	659	OMG	C3'-C4'-C5'-O5'
1	Aa	913	OMG	O4'-C4'-C5'-O5'
27	BA	61	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

22 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	BA	1949	OMU	3	0
27	BA	879	A2M	1	0
27	BA	912	OMG	1	0
1	Aa	5	4AC	1	0
1	Aa	918	LV2	1	0
27	BA	2672	OMG	1	0
27	BA	2379	OMG	2	0
27	BA	674	OMG	1	0
27	BA	1623	OMU	1	0
27	BA	61	A2M	1	0
1	Aa	458	4AC	4	0
1	Aa	917	5MU	1	0
27	BA	2353	OMG	1	0
27	BA	2745	OMG	1	0
1	Aa	730	4AC	1	0
27	BA	2115	OMG	2	0
1	Aa	1449	6MZ	1	0
1	Aa	1459	4AC	2	0
27	BA	505	A2M	2	0
27	BA	1945	OMG	1	0
27	BA	869	OMC	1	0
27	BA	2120	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
27	BA	1
7	Ag	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	582:A	O3'	583:A	P	4.39
1	Ag	75:ASP	C	76:SER	N	3.06

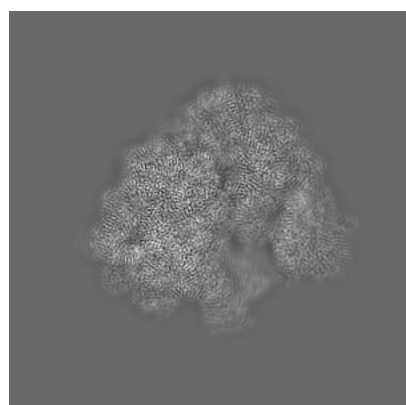
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10503. These allow visual inspection of the internal detail of the map and identification of artifacts.

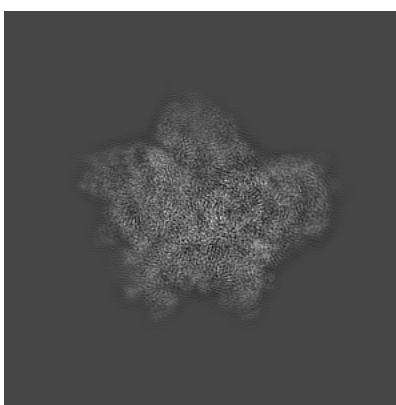
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

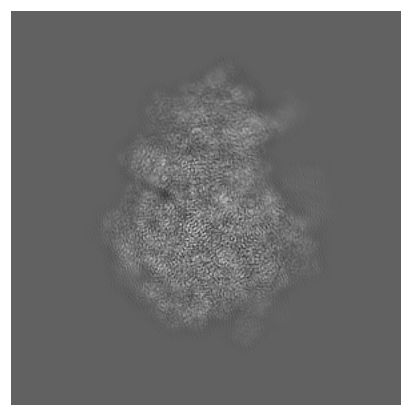
6.1.1 Primary map



X



Y

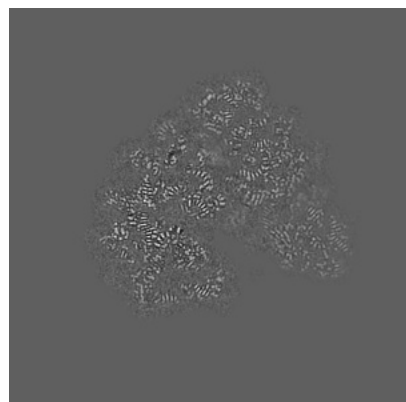


Z

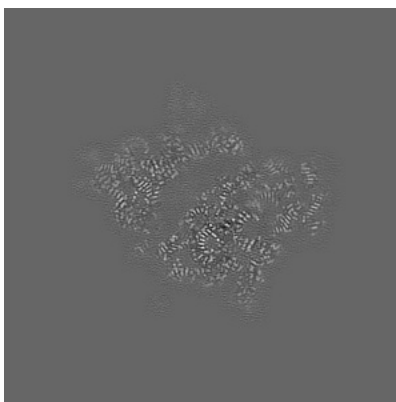
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

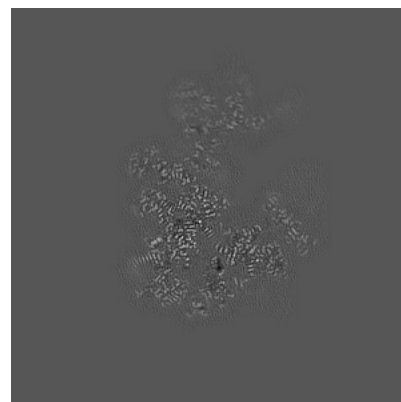
6.2.1 Primary map



X Index: 240



Y Index: 240

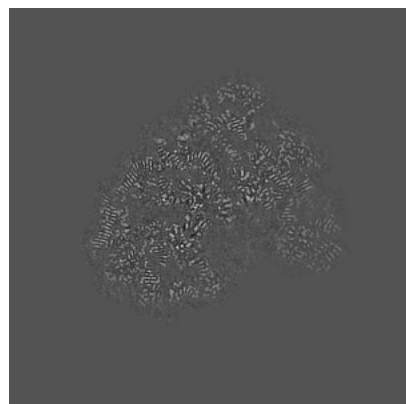


Z Index: 240

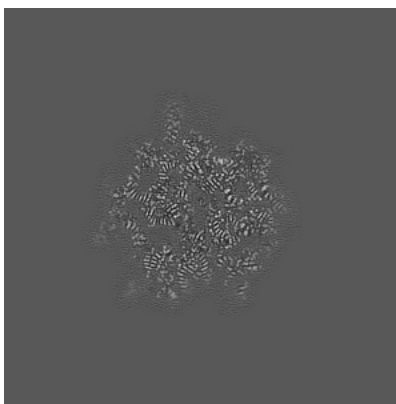
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

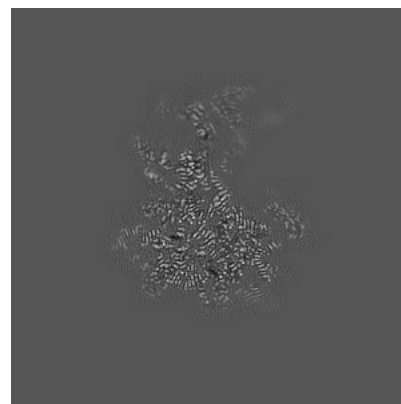
6.3.1 Primary map



X Index: 227



Y Index: 181

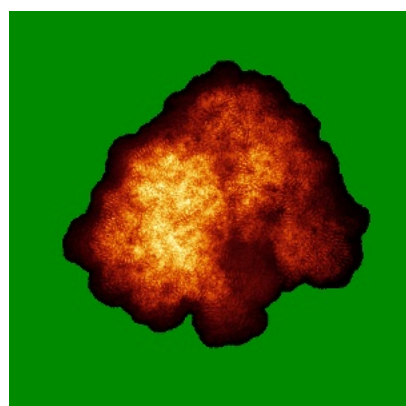


Z Index: 265

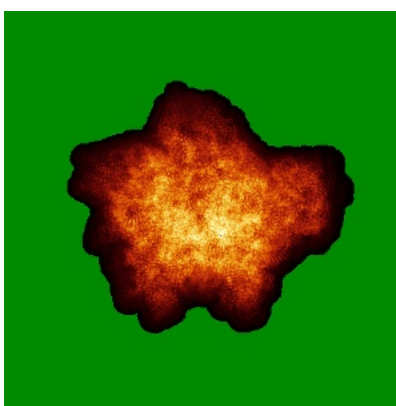
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

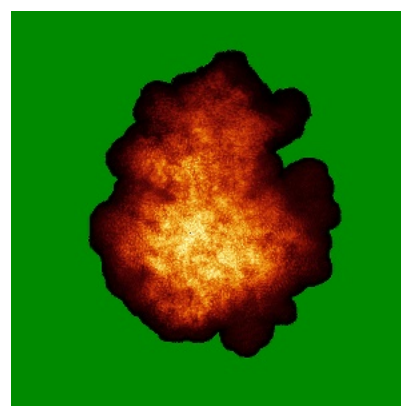
6.4.1 Primary map



X



Y

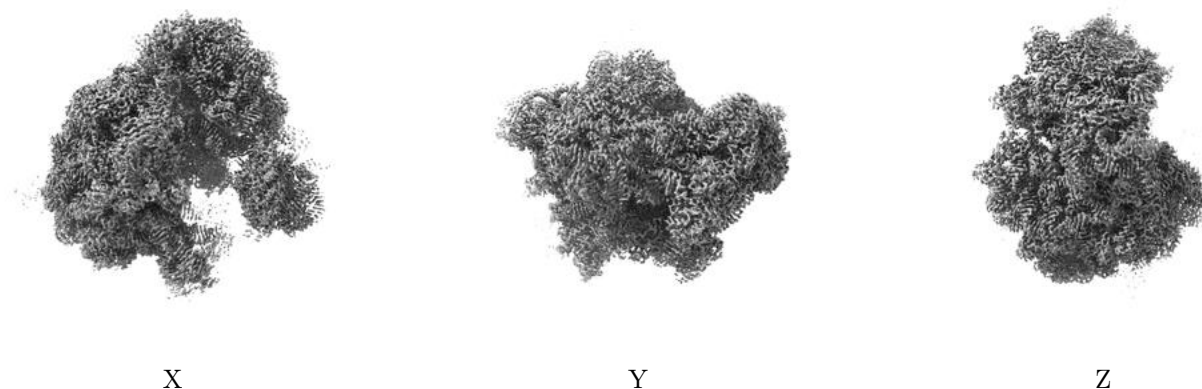


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

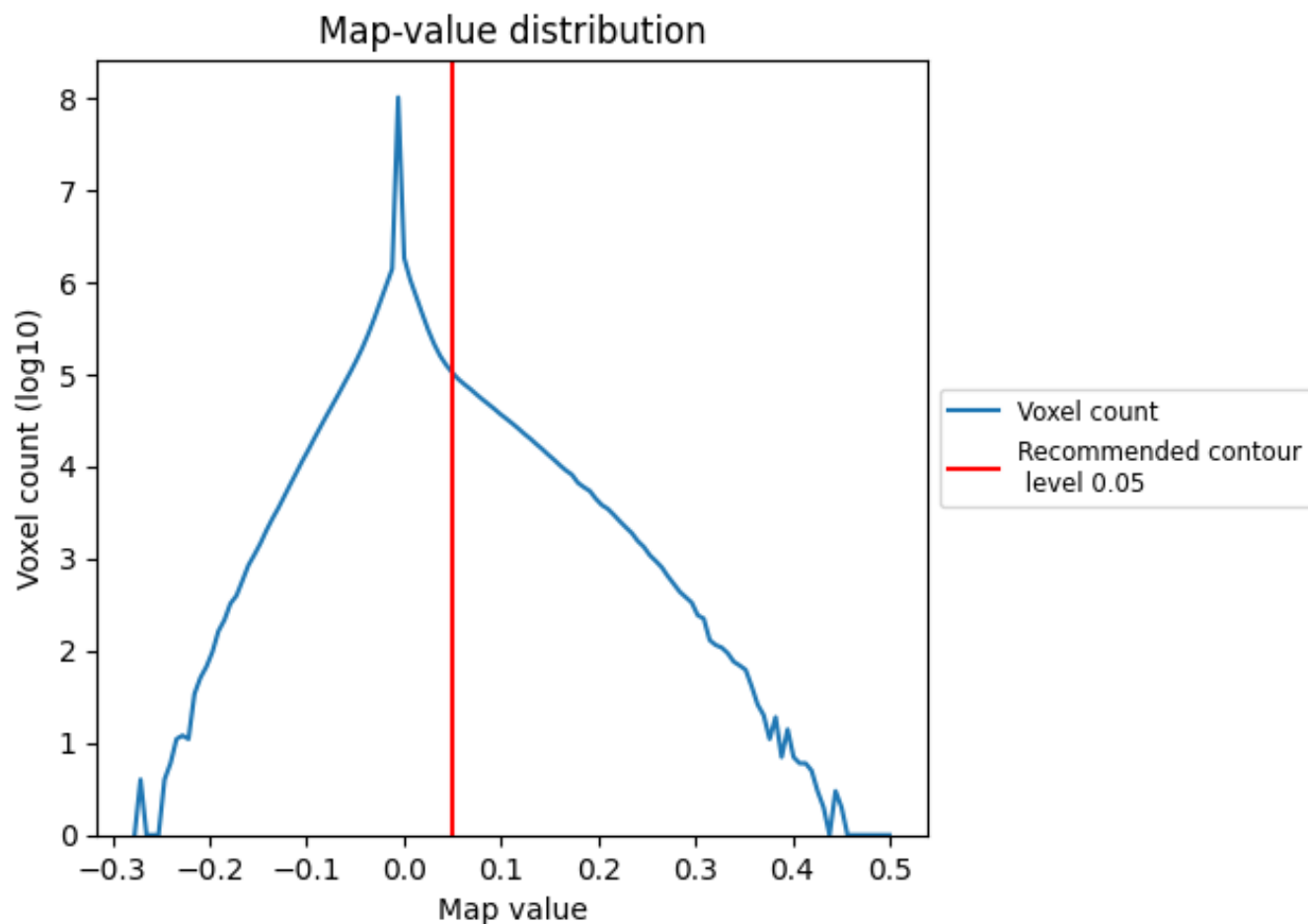
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

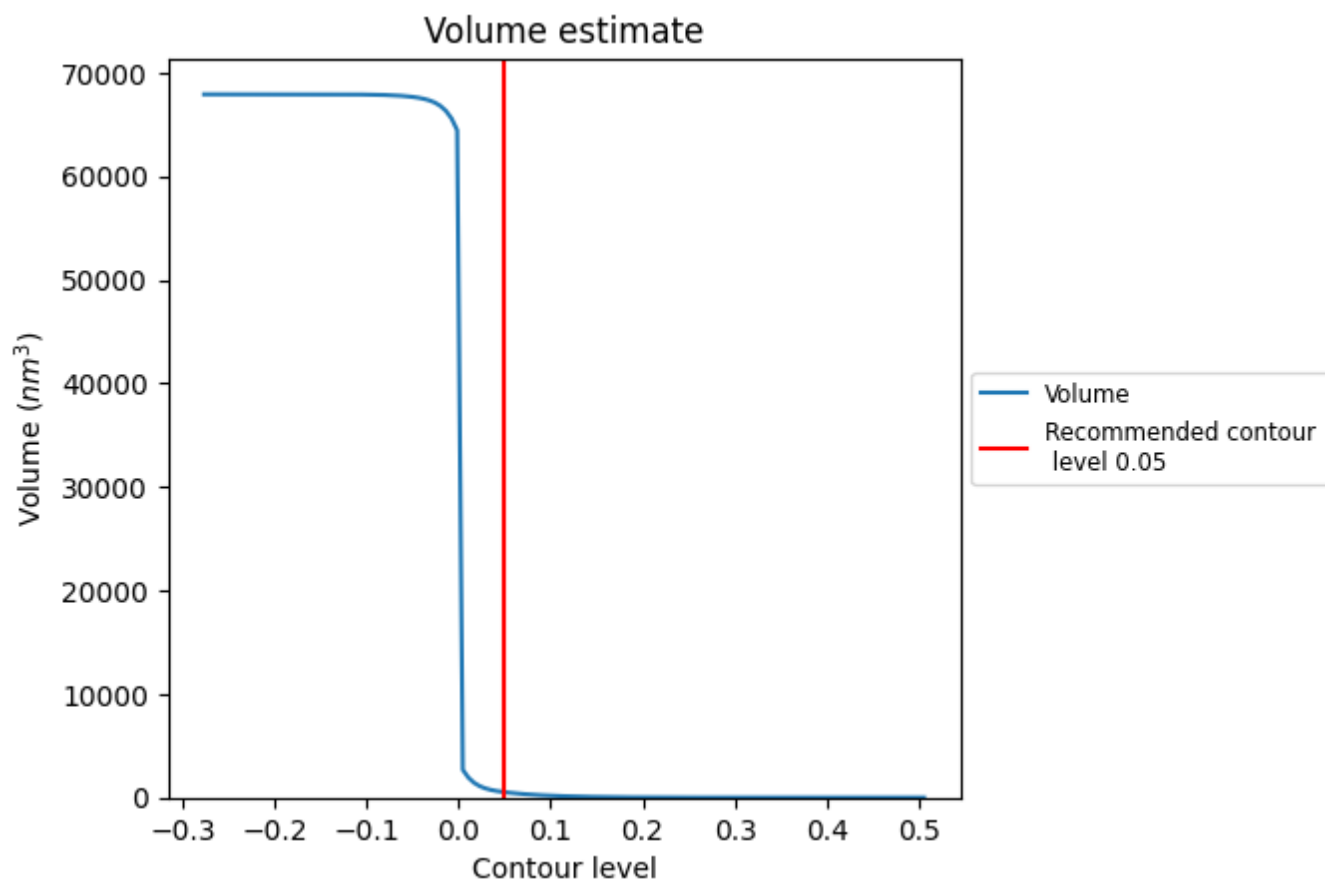
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

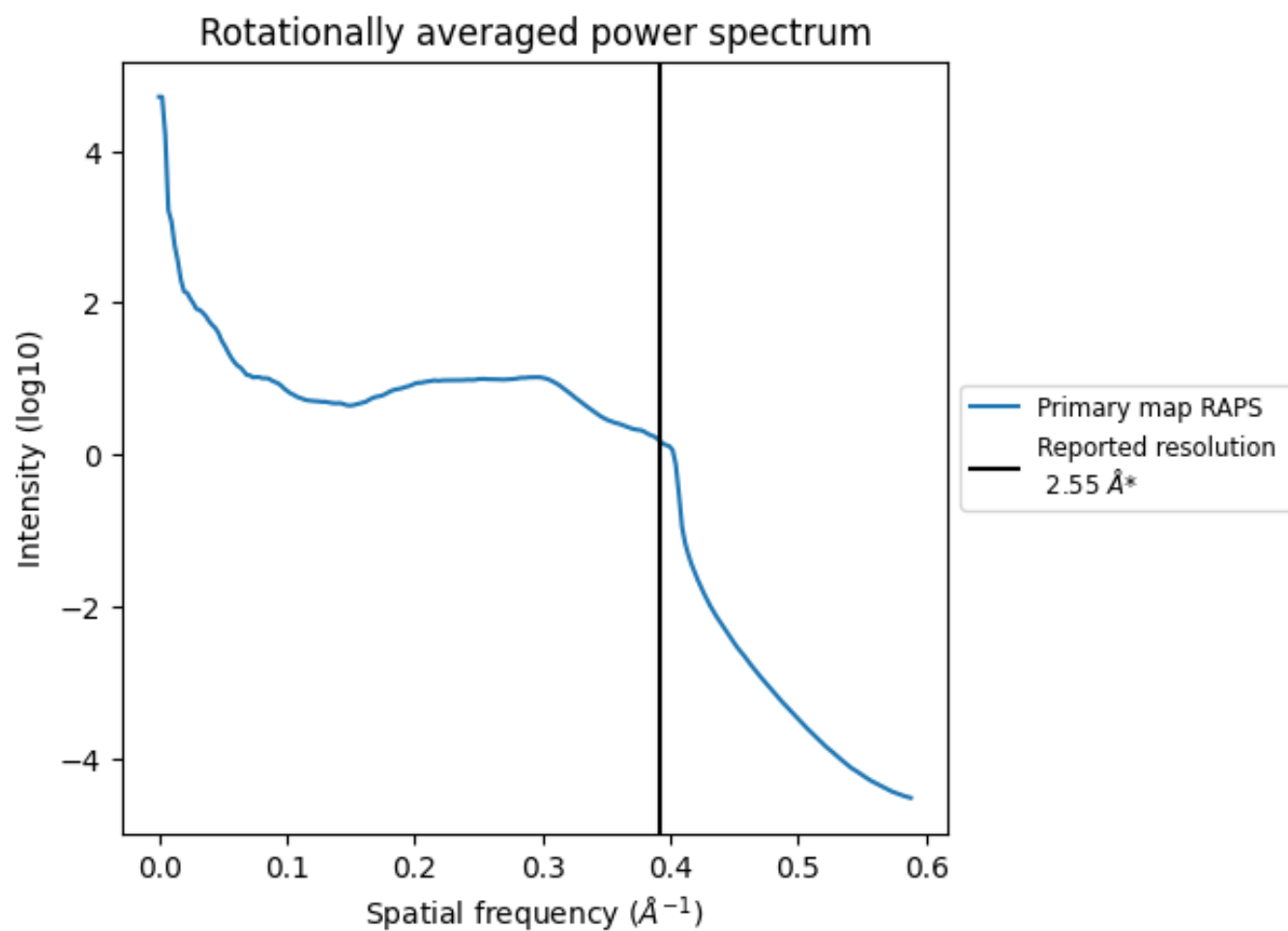
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 518 nm³; this corresponds to an approximate mass of 468 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.392 Å⁻¹

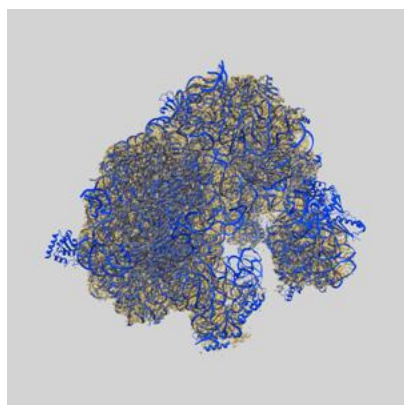
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

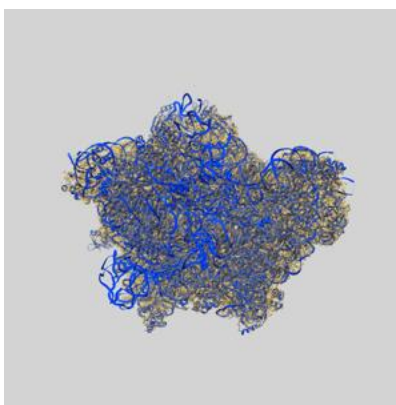
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-10503 and PDB model 6TH6. Per-residue inclusion information can be found in section 3 on page 18.

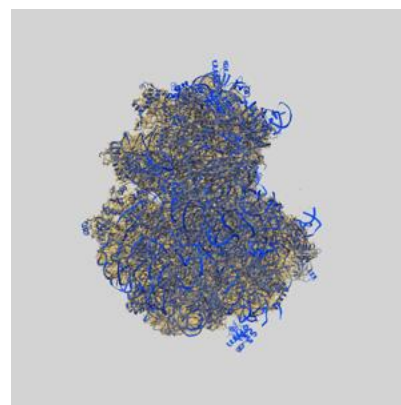
9.1 Map-model overlay ⓘ



X



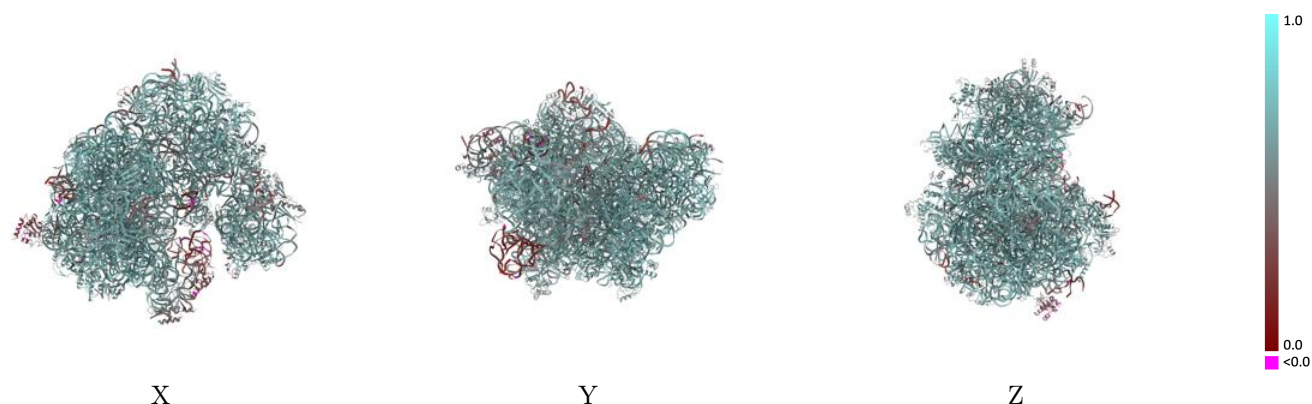
Y



Z

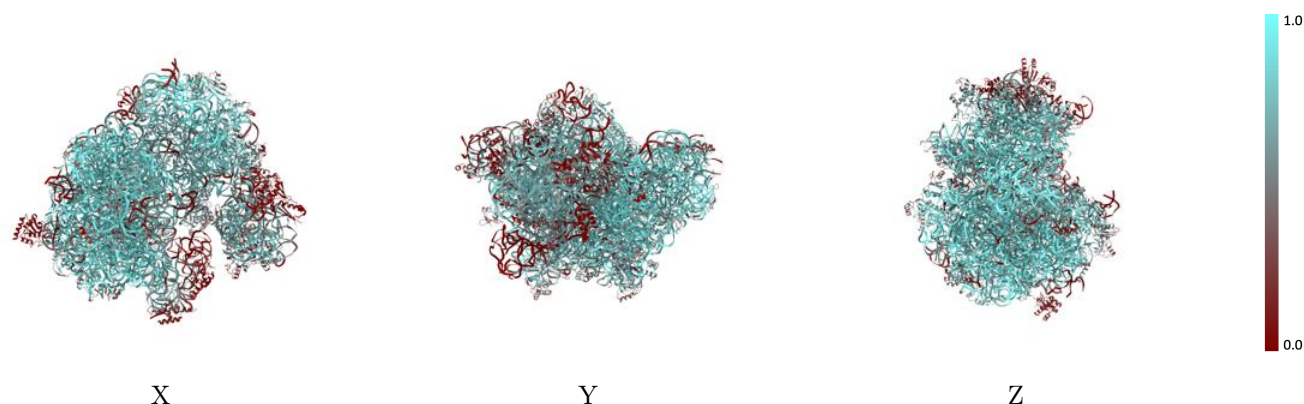
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



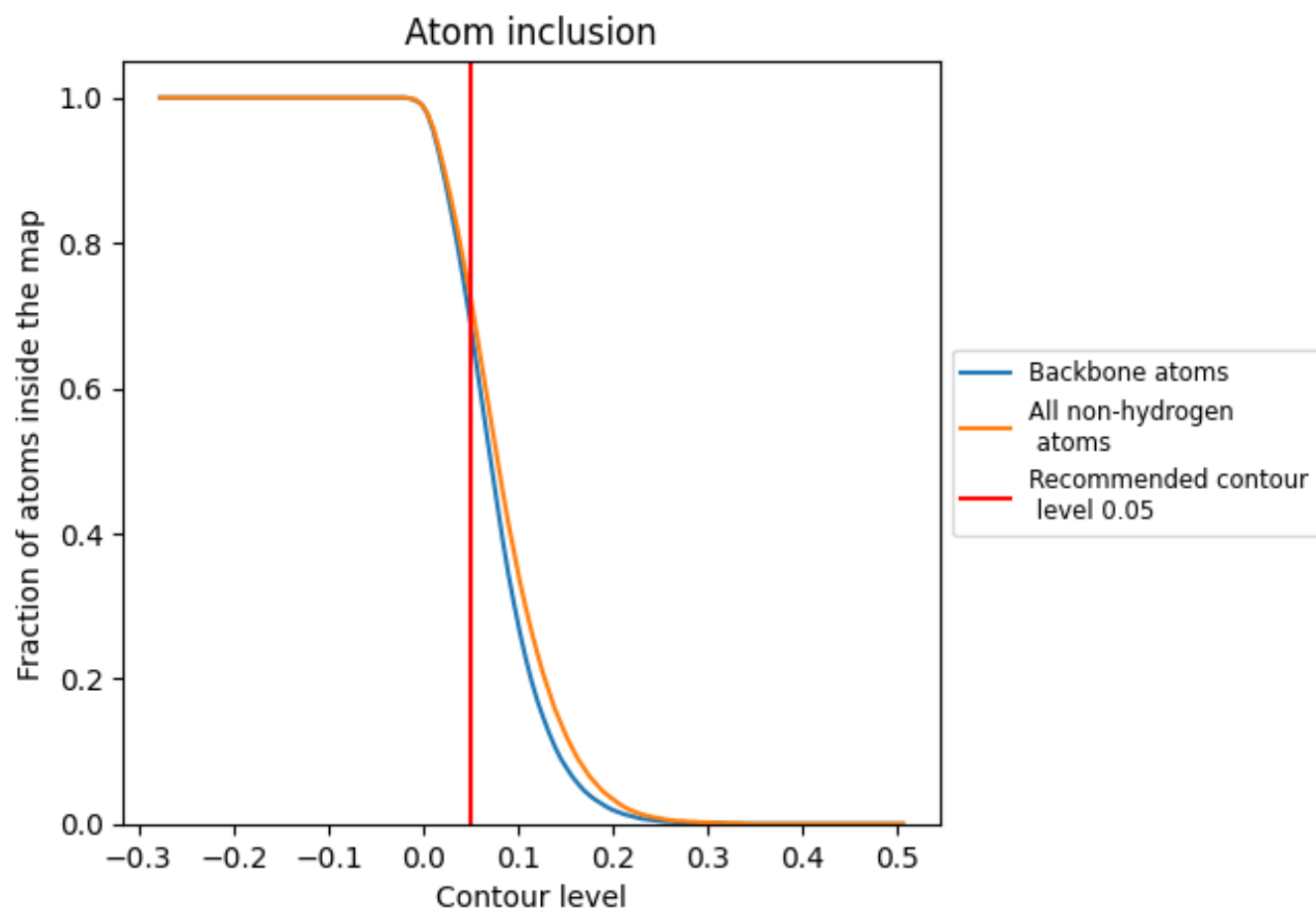
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.6220
Aa	 0.7550	 0.6320
Ab	 0.5560	 0.6270
Ac	 0.1560	 0.5370
Ad	 0.5400	 0.6070
Ae	 0.6830	 0.6450
Af	 0.7640	 0.6520
Ag	 0.7200	 0.6340
Ah	 0.3250	 0.5650
Ai	 0.4630	 0.5940
Aj	 0.7980	 0.6580
Ak	 0.7300	 0.6350
Al	 0.5050	 0.6260
Am	 0.2270	 0.5540
An	 0.5050	 0.6120
Ao	 0.7050	 0.6510
Ap	 0.4540	 0.5650
Aq	 0.7170	 0.6350
Ar	 0.4240	 0.5780
As	 0.5790	 0.5960
At	 0.0350	 0.5090
Au	 0.4660	 0.6130
Av	 0.5750	 0.6340
Aw	 0.5660	 0.6110
Ax	 0.6150	 0.6110
Ay	 0.2680	 0.5710
Az	 0.7060	 0.6440
BA	 0.8080	 0.6240
BB	 0.5070	 0.5460
BC	 0.8580	 0.6730
BD	 0.8420	 0.6770
BE	 0.8270	 0.6680
BF	 0.1190	 0.3620
BG	 0.5790	 0.6030
BH	 0.5470	 0.5880



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Chain	Atom inclusion	Q-score
BI	 0.0010	 0.3030
BJ	 0.6400	 0.6170
BK	 0.8160	 0.6720
BL	 0.7960	 0.6530
BM	 0.5930	 0.5990
BN	 0.4260	 0.5440
BO	 0.6060	 0.6120
BP	 0.8920	 0.6800
BQ	 0.4630	 0.5670
BR	 0.7930	 0.6570
BS	 0.8370	 0.6620
BT	 0.5550	 0.6250
BU	 0.8450	 0.6780
BV	 0.8610	 0.6740
BW	 0.7250	 0.6410
BX	 0.7810	 0.6450
BY	 0.7700	 0.6460
BZ	 0.5780	 0.5810
Ba	 0.7890	 0.6560
Bb	 0.6060	 0.5970
Bc	 0.7770	 0.6660
Bd	 0.8160	 0.6700
Be	 0.8170	 0.6530
Bg	 0.7970	 0.6600
Bh	 0.9420	 0.6990
Bi	 0.7720	 0.6250
Bj	 0.6970	 0.6420
Bk	 0.8770	 0.6490
Bl	 0.7700	 0.6600